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Sequence:
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 14, 2003, 18:28:36; search time 35 Seconds (without alignments) 102.793 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908470 seqs, 133250620 residues
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120
1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
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1: /SIDS2/gcgdata/
2: /SIDS2/gcgdata/
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

10	9	8	7	O	S	4	ω	N	1	Result
120	120	120	120	120	120	120	120	120	120	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
27	27	27	27	27	27	27	27	27	27	Length DB
22	22	22	22	22	22	22	22	22	18	DB
AAU10204	AAU10203	AAU10202	AAU10201	AAU10200	AAU10199	AAU10197	AAU10196	AAU10195	AAW35723	D
Snail Kappa-conoto	Kappa-conotoxin PV	Description								

<b>4</b> -	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
77	77	77	77	77	77	77	77	81	81	81	81	81	81	81	81	81	81	81	112	112	112	112	112	114	114	115	115	116	117	120	120	120	120	120
64.2	64.2	64.2	64.2	64.2	64.2	64.2	64.2	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67.5	93.3	93.3	93.3	93.3	93.3	95.0	95.0	95.8	95.8	96.7	97.5	100.0	100.0	100.0	00	100.0
26	26	26	26	26	26	26	26	30	26	26	26	26	26	26	26	26	26	26	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
21	21	20	19	18	18	14	14	23	23	22	21	21	20	19	18	18	14	14	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22
AAY56480	AAB14359	AAW95571	AAW72612	AAW12974	AAW19551	AAR39615	AAR37760	ABB96679	ABB96887	AAB19462	AAY56496	AAB14370	AAW95584	AAW72625	AAW12985	AAW19570	AAR39628	AAR37774	AAU10219	AAU10215	AAU10213	AAU10211	AAU10209	AAU10216	AAU10210	AAU10214	AAU10198	AAU10217	AAU10212	AAU10218	AAU10208	AAU10207	AAU10206	AAU10205
Natural omega cono	Omega-conopeptide	Omega-conopeptide	Conus genus natura	Omega conopeptide	Natural omega-cono	SVIB/SNX183. Synt	SVIB/SNX-183. Syn	Omega-conopeptide	Omega-conopeptide	Sequence of an ome	Analogue omega con	Omega-conopeptide	Analog omega-conop	Conus genus analog	Omega conopeptide	SNX-202, omega con	SNX-202. Syntheti	SNX-202. Syntheti	Snail Kappa-conoto	-	-	_	Snail Kappa-conoto	ب	Snail Kappa-conoto	_		Snail Kappa-conoto	_	_		Snail Kappa-conoto		Snail Kappa-conoto

## ALIGNMENTS

PR	PF	PD	ХХ	XX	H.	ijij	FT	FT.	ΕT	ΗŦ	Ŧ	FH .	X C	×	ΚW	XW	XE	X	Dī	XX	ĕ X	RESULT 1 AAW35723 ID AAW
18-MAR-1996;	14-MAR-1997;	25-SEP-1997.	W09734925-A1.		production bond	pion file bond	Disulfide-bond	Disulfide-bond			Modified-site	<del>;</del> кеу	conus purpurascens		cone snail; yen	Kappa-conotoxin	Kappa-conocoxin PVIIA	•	03-APR-1998 (f:		AAW35723;	LT 1 5723 AAW35723 standa
96US-0619936.	97WO-US03483.				/note= "disulphide bond"	/note= "disulphide bond"		116 /note= "disulphide bond"	hydroxyproline or proline"	<pre>/note= "Optionally 4-trans-hydroxyproline,</pre>	4	Location/Qualifiers	eis.		<pre>cone snail; yenom; goldfish; delta-conotoxin PVIIA; disulphide.</pre>	<pre>Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release;</pre>	PVIIA.		(first entry)			7 1 723 AAW35723 standard; peptide; 27 AA.

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RESULT 2
AAU10195
ID AAU1
XX AAU1
AC AAU1
XX AAU1
AC Snai
XX Purp
KW Purp
KW card
XX Conu
OS Conu
OS Synt
XX Synt
XX Misc
FT Misc
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a new kappa-conotoxin PVIIA which targets potassium channels and can be used to augment neurotransmitter release in pathological situations such as autoimmune diseases, e.g. Alzheimer's disease, Lambert-Eaton syndrome or myasthenia gravis. This peptide together with delta-conotoxin PVIIA act synergistically to rapidly immobilize fish which are injected with the two peptides. Injection of kappa-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This "fin-popping" occurs repeatedly resulting in a series of jerky movements, but injection of only kappa-conotoxin PVIIA does not immobilize or kill the fish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus purpurascens Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New kappa-conotoxin peptides - which target potassium channels and can be used to augment neurotransmitter release in e.g. autoimmune
                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snail Kappa-conotoxin PVIIA analogue #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU10195 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     any
                    /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho O-phospho-Tyr, nitro-Tyr, (D,L)-Trp, neo-Trp
                                                                                                                                               /label= OTHER
/label= OTHER
/note= "Other= Arg, homoArg, orn
/note= "Other= Arg, homoArg, homoAr
                                                                                                                                                                                                                                                                                                                                                                           N-methyl-Lys,
any synthetic
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N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trime
any synthetic basic amino acid, His or halo
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(D,L)-halo-Trp"
                                                                                                         /label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= OTHER
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Pred. No. 0.00036;
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                                                                                                                                                                                                                                                                                           or Hydroxyproline"
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His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                 N,N,N-trimethyl-Lys
His or halo-His"
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Matches Query Match Best Local

Similarity 27; Conser

100. ilarity 100. Conservative

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Score 120; DB 22; Pred. No. 0.00036; ; Mismatches 0;

Indels Length

Gaps

0;

27; 0;

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                                                                  The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebrai ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin
                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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Sequence
                                                                                                                                                                                                                                                                                                                   Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cornell-Bell AH,
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20-JUL-2000;
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                                               analogue
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27
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2000US-0219438.
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N-methyl-Lys, N.N-dimethyl-Lys,
any synthetic basic amino acid,
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr, (D,L)-Trp, neo-Trp or (D,L)-halo-Trp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    any synthetic
19
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or an amide ~~~~"
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N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys,
any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Other= Arg, homoArg, ornithine, Lys,
N-methyl-Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys,
any synthetic basic amino acid, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- OTHER
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                                                                                                                                                                                                                                                                                                             46pp;
                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pemberton
                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Other=
                                                                                                                                                                                                                                                                                                                   English.
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ys, N,N,N-trimethyl-Lys,
id, His or halo-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Layer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT;
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RESULT 3
AAU10196

AAU10196 standard; peptide;

27

A

cardioactive; antias cerebral ischaemia;

Synthetic

Conus purpurascens

WO200121648-A1

Modified-site Modified-site

/note= 27

"Hyroxyproline"

Location/Qualifiers

/note= "The C-terminus or an amide group"

29-MAR-2001.

Snail Kappa-conotoxin PVIIA analogue R18A

16-JAN-2002 AAU10196

(first entry)

Ъ

CXIXNQXCXQXLDDCCSXXCNXXNXCV

27

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              ρy
                                Matches
                                        Query Match
Best Local
                                                                                         The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, coular ischaemia and asthma. The present sequence is a kappa-conotoxin
                                                                 Sequence
                                                                                                                                                                    Claim 1; Page 27; 46pp; English.
                                                                                 PVIIA analogue of the invention
               ш
        CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                               18; Conservative
                                                                  27
                                                                 A
A
                                        100.0%;
                                9;
                                       Score 120;
Pred. No. 0.
                                Mismatches
                                        DB 22;
                                0
                                               Length
                                Indels
                                                 27;
                               0,
                               Gaps
                               0
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0

RESULT 5

XXX Ħ

AAU10199;

AAU10199

standard; peptide;

27

B

kappa-conotoxin PVIIA peptide -

WPI; 2001-648090/74.

Cornell-Bell AH,

Pemberton KE,

Temple DL,

Layer RT,

(COGN-) COGNETIX INC.

22-SEP-1999; 99US-155135P. 20-JUL-2000; 2000US-0219438. 21-SEP-2000; 2000WO-US25827

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Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; R18A.
                                                                                                                                                                                                                     Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is either a carboxyl group
                                                                                                                                                                                                                                                                                                                                     McCabe RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10197
                                                              XXXXX
Best Loc
Matches
                              Query Match
                                                                                                                        The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
                                                                                                                                                                                                                                                     Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                   Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                 Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-SEP-1999; 99US-155135P.
20-JUL-2000; 2000US-0219438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebral ischaemia; ocular ischaemia; asthma; R22A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purple cone snail; kappa-conotoxin PVIIA analogue; circardioactive; antiasthmatic; KATP channel activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snail Kappa-conotoxin PVIIA analogue R22A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU10197 standard; peptide;
                                                              Sequence
                                                                                           ischaemia and asthma. PVIIA analogue of the
                                                                                                                                                                                                                                                                                       kappa-conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                                   Jones
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               Local
 l Similarity
18; Conser
                                                            27 AA;
 Conservative
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "The C-terminus is either a carboxyl group
                                                                                                                                                                                                                                                                                                                                                                                                                    Pemberton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an amide group'
             100.0%; Score 120; DB 22
66.7%; Pred. No. 0.00036;
                                                                                             The present sequence is a invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
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 Pred. No. 0.0
9; Mismatches
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                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                  Layer RT,
                                                                                                            kappa-conotoxin
                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circulatory;
 Indels
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                                 27;
 0,
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 Gaps
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RESULT 6
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                   The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin
                 Snail Kappa-conotoxin PVIIA
                                                                                                                                                                                                                                                                                                      Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                      Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebral ischaemia; ocular ischaemia; asthma; K19A.
 Purple cone snail;
                                                                        AAU10200 standard;
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-648090/74.
                                                                                                                                                                                                                                                                                                                                                                                         Jones
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                                     16-JAN-2002
                                                       AAU10200;
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20-JUL-2000;
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                                                                                                                                                                 Local
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                                                                                                                                       1 CXTXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                     CRIXNQKCFQHLDDCCSRACNRFNKCV 27
                                                                                                                                                                                                             analogue
                                                                                                                                                         1 Similarity
18; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    snail; kappa-conotoxin PVIIA analogue; circulatory;
e; antiasthmatic; KATP channel activation; cardiac ischaemia;
                                                                                                                                                       100.0%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-155135P
2000US-0219438
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27
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                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton
 kappa-conotoxin PVIIA analogue; circulatory;
                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an amide group"
                                    entry)
                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Hyroxyproline"
                                                                                                                                                        ; Score 120; DB 22; Pred. No. 0.00036; 9; Mismatches 0;
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                  analogue R2A.
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                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                 RT,
                                                                                                                                                                                                                                                                                                                                an individual a
                                                                                                                                                                                                                                                                                                                                                                                                 McCabe
                                                                                                                                                                           27;
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AAU10201
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Conus purpurascens Synthetic.
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                                                                                  16-JAN-2002
                                                                                                   AAU10201;
                                                                                                                    AAU10201 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornell-Bell AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                              Local
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                                                                                                                                                                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                 CAIXNQKCFQHLDDCCSRKCNRFNKCV
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cardioactive; antiasthmatic; KATP channel activation; cerebral ischaemia; ocular ischaemia; asthma; R2A.
                                       cardiac ischaemia;
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# Conus purpurascens Synthetic.

Location/Qualifiers "Hyroxyproline"

/note= /note= ote= "The C-terminus an amide group" is either a carboxyl group

22-SEP-1999; 99US-155135P 20-JUL-2000; 2000US-0219438

(COGN-) COGNETIX INC

Pemberton KE, Temple DL, Layer RT, McCabe RT

WPI; 2001-648090/74.

Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide

Claim 1; Page 27; 46pp; English.

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, coular ischaemia and asthma. The present sequence is a kappa-conotoxin analogue of the invention.

ĄΑ,

18; Conser Conservative 100.08; Pred. No. 0.0
9; Mismatches Score 120; Pred. No. 0 J.00036; 0; Indels Length 27; 0; Gaps

0;

27

peptide; 27

ζ

(first entry)

Snail Kappa-conotoxin PVIIA analogue F9A

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; F9A.

carboxyl group

RT,

McCabe RT;

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Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 27; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cornell-Bell AH, Pemberton
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Modified-site
                                                                                                            Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K25A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-648090/74.
                                                                    Conus purpurascens Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kappa-conotoxin PVIIA peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones
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                               Modified-site
                                                                                                                                                                   Snail Kappa-conotoxin PVIIA analogue K25A
                                                                                                                                                                                                16-JAN-2002
                                                                                                                                                                                                                                                       AAU10202 standard;
                                                                                                                                                                                                                                                                                                                        l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                (first entry)
/note=
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                                        Location/Qualifiers
                                                                                                                                                                                                                                                     peptide;
                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                ; DB 22;
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nes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 27; 46pp; English.
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20-JUL-2000;
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                                                                                                                                        Conus purpurascens.
                                                                                                                                                                                  Purple cone snall; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K2K.
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2000US-0219438
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or an amide group"
                                          /note= "The C-terminus is or an amide group"
                                                                                                            Location/Qualifiers
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Pred. No. 0.00036;
9; Mismatches 0;
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RESULT 10
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a fART channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin
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20-JUL-2000; 2000US-0219438
     22-SEP-1999;
                                  21-SEP-2000; 2000WO-US25827
                                                                     29-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU10204 standard; peptide;
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     990S-155135P
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                                                                                                                                   /note= "The C-terminus is either a carboxyl group
or an amide group"
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Matches 18
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 Cornell-Bell AH,
                                (COGN-) COGNETIX INC
                                                               22-SEP-1999;
20-JUL-2000;
                                                                                                                   21-SEP-2000; 2000WO-US25827
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1 Similarity 66.7%;
18; Conservative 9
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                                                                   2000US-0219438.
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Pemberton KE,
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20-JUL-2000; 2000US-0219438.
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Treating disorders associated with
                        WPI; 2001-648090/74.
                                                                                                                                              21-SEP-2000; 2000WO-US25827.
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membrane e.g. cardiac, cerebral and comprises activating a KATP channel kappa-conotoxin PVIIA peptide -
                                                                                                  ocular ischaemia
by administering
                                                                                                    and asthma
to an individual a
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Claim 1; Page English.

The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, coular ischaemia and asthma. The present sequence is a kappa-conotoxin Sequence PVIIA analogue of the invention. 27 AA;

بعيد

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Query Match
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Matches 18
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nes 18; Conser
1 CRIXNQKCYQHLDDCCSRKCNRENKCV 27
                      1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                            Conservative
                                                    100.0%;
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; Pred. No. 0.00036;
9; Mismatches
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Вb Š

RESULT 13
AAU10207
ID AAU10 16-JAN-2002 AAU10207; AAU10207 standard; peptide; (first entry) PVIIA analogue 27 Å

Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac i cerebral ischaemia; ocular ischaemia; asthma; R2Q. ischaemia;

Conus purpurascens. Synthetic. Modified-site Location/Qualifiers "Hyroxyproline"

Modified-site /note= 27 /note= "The C-terminus is either a carboxyl group or an amide group"

WO200121648-A1

29-MAR-2001.

21-SEP-2000; 2000WO-US25827

PANCH CANAL 22-SEP-1999; 20-JUL-2000; 99US-155135P. 2000US-0219438.

(COGN-) COGNETIX INC

Cornell-Bell Jones AΗ, Pemberton XΕ, Temple DL, Layer 眔 McCabe RT;

WPI; 2001-648090/74.

Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide individual a

Claim 1; Page 28; 46pp; English

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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; HILA.
                                                                Claim
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20-JUL-2000;
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or an amide group"
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       depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and astima. The present sequence is a kappa-conotoxin
                                                                                                                           Claim 1; Page 28; 46pp; English.
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                                                                                                  invention relates to treating
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-619-936-1
US-08-049-734-19
US-08-049-794-19
US-08-049-74-19
US-08-67-774-19
US-08-67-354-19
US-08-613-400A-19
US-08-613-400A-19
US-08-613-400A-19
US-08-613-400A-19
US-08-613-400A-19
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US-08-613-400A-8
US-08-613-400A-8
US-08-613-400A-8
US-08-613-400A-8
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US-08-613-400A-8
US-08-613-400A-8
US-08-185-432-18
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56.7	56.7	56.7	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5
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US-08-532-384-20	US-08-083-590A-20	US-08-185-432-17	US-08-092-215-9	US-09-392-979A-29	US-09-392-979A-21	US-09-298-017-29	US-09-298-017-21	US-08-613-400A-29	US-08-613-400A-21	US-09-138-439-29	US-09-138-439-21	US-08-965-918-29	US-08-965-918-21	US-08-675-354-29	US-08-675-354-21	US-08-742-774-29	US-08-742-774-21
Sequence 20, Appl	Sequence 20, Appl	Sequence 17, Appl	Sequence 9, Appli	29,	Sequence 21, Appl	29,					21,						

ALIGNMENTS

	5 - Si 2 - Si 3 - Si
NUMBER OF INVENTION: CONCENT PEPLIGE PVIIA NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC COUNTRY: U.S.A. ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTUMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/619,936 FILING DATE: CLASSIFICATION NUMBER: US/08/619,936 FILING DATE: CLASSIFICATION NUMBER: 38,609 RECISTRATION NUMBER: 38,609 RECISTRATION NUMBER: 38,609 RECISTRATION NUMBER: 24260-107674-04 TELECOMMUNICATION INFORMATION: NAME: SAXe, Stephen A. RECISTRATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 27 amino acids TYPE: ADDRES: Single TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ORGANISH: Conus purpurascens PEATURE: NOAME/KEY: Modified-site LOCATION: 4 COTHER INFORMATION: /product= "Ahyp" OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline." FEATURE: NAME/KEY: Modified-site LOCATION: 4 COTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."	n US/08619936  Heinrich i-Joon , Michelle , Baldomero M.

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RESULT 2
US-07-789-913-19
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; LOCATION:
US-08-619-936-1
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Best Local Similarity 66.7%;
Matches 18; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19,
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                              TELEFAX: (415) 324-0960 NFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION UDATA:
APPLICATION UNBER: US 07/440,094
FILING DATE: 22-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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                                ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: UPFILING DATE: 19911112
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                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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               NDIVIDUAL ISOLATE: SNX-202
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Valentino, Karen L.
Bitner, Robert S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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Pred. No. 4
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                             RESULT 4
US-08-496-847-19
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Sequence 19, Application US/08496847 Patent No. 5795864
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RESULT 3
US-08-049-794-19
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                                                                                 Query Match
Best Local
                                                                                                                                                                                                                             TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM DC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WILLJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
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                                                                                                                                                INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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CKLKGQSCSRLMYDCCSGSCGRSGKC 26
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                                                                Conservative
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                                                                                 67.5%;
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                                                               Score 81; DB 1
Pred. No. 0.14;
l3; Mismatches
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                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                    PPLICANT: SINGH, TELLING APPLICANT: SINGH, TELLING APPLICANT: GOHIL, KISHOR C APPLICANT: VALENTINO, KAREN L APPLICANT: MILJANICH, GEORGE P APPLICANT: MILJANICH, GEORGE P APPLICANT: MILJANICH, GEORGE P APPLICANT: MILJANICH, GEORGE P APPLICANTION: METHODS OF PRODUCING ANALGESIA AND THE THE APPLICANTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
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OMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                   COUNTRY: USA
ZIP: 94306
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                                                                                        350 Cambridge Avenue,
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                                                                                        Law Offices of Peter Dehlinger 0 Cambridge Avenue, Suite 300
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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE
US-08-742-774-19
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Best Local Similarity
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LENGTH: 26 amino acids
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                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
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                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/6 FILING DATE: 03-JUL-1996
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REFERENCE/DOCKET NUMBER: 5865-0009.30
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                                     CLASSIFICATION:
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                                                APPLICATION NUMBER: US/08/675,354 FILING DATE: 03-JUL-1996
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APPLICATION NUMBER:
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GOHIL, KISHOR C
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                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
ANAME: MODIT, JUCY M.
REGISTRATION NUMBER: 38,563
REFERENCE/POCKET NUMBER: 5865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650,324-0880
                                                                                      NFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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LENGTH: 26 amino acids
                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    SOFTWARE: FASTSED for Windows Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
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MEDIUM TYPE: Diskette
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      HYPOTHETICAL:
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VENTION: METHODS AND F
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for Windows Version
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APPLICATION NUMBER: US/08,
FILING DATE: 193-04-15
APPLICATION NUMBER: US 07,
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                      TELEFAX: (415) 324-096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               MOLECULE TYPE: HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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                                                         Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                             NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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                           1 CXIXNOXCXOXLDDCCSXXCNXXNXC 26
                                                                                                                                                                                                                         LENGTH:
1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
                                                                                                                                  INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
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5994305
                                                                                                                                                                                             amino acid
)GY: linear
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                                                                                                                                                                                                                                                              (415)
(415) 37
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                                                                                                                                                                                                                           26 amino acids
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                    324-0960
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34.6%;
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                                                                                                                                                                                                                                                                                                  34,444
FR: 5865-0009.30
                                                          13;
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                                                         Score 81; DB 2
Pred. No. 0.14;
13; Mismatches
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Pred. No. 0.14;
13; Mismatches
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                                                                                     Length 26;
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US-08-613-400A-19
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US-09-298-017-19
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                                                                                                                                                      Patent No.
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                         GENERAL INFORMATION:
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HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                       APPLICANT:
APPLICANT:
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NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: U
FILING DATE: 08-MAR-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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             APPLICANT: MILJANICH, GEORGE P
TITLE OF INVERTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                             Local Similarity 34.0 es 9; Conservative
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                                                                                                                                                                                                                                                  1 CKLKGQSCSRLMYDCCSGSCGRSGKC 26
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                                                                                                                                                                     19, Application US/09298017
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                                                                      SINGH, TEJINDER
GOHIL, KISHOR C
VALENTINO, KAREN L
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                                                                                                                      JUSTICE, ALAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                        : protein
NO
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METHOD OF PRODUCING ANALGESIA
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Pred. No.
                                                                                                                                                                                                                                                                                                              Mismatches
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INDIVIDUAL ISOLATE: SNX-202, FIGURE US-09-298-017-19
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US-09-392-979A-19
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL:
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LENGTH: 26 amino acids
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                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICATION NUMBER:
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                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                               APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                         STREET: 350 Camp
CITY: Palo Alto
                                                                                                                              COUNTRY:
APPLICATION NUMBER: US/09/392,979A
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                                                                                                                  94306
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350 Cambridge Avenue, Suite 300
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                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No.
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0.14;
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                               #1.25
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RESULT 12
US-07-789-913-8
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Patent No. 5559095
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
ETILING DATE: 02-NUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
ETILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
BEGTTGRATTON NUMBER: 34.444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
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FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 5865-0009.30
REFERENCE/TOOK INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYTILE OF INVENTION: Delayed Treatment method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
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ZIP: 94306
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                                                                                                                                                                                        CLASSIFICATION:
REFERENCE/DOCKET NUMBER: 5865-0005.30
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Valentino,
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                                                                                           US 07/440,094
                                                                                                                                                  US 07/561,766
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                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPEE: ANYMO ACTO
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Patent No. 5
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/049,794
ETLING DATE: 1930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
ETLING DATE: 30-DEC-1991
ATTORNEY/AGENT IMPORMATION:
NAME: Stratford, Carol A.
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TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1
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HYPOTHETICAL: N
ANTI-SENSE: NO
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LENGTH: 26 amino acids
TYPE: AMINO ACID
                  MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WILLJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPINTE ANALGESIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARDE: PC-TOS/MS-DOS
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                                                                                                                                                                                                                                               NAME: Stratford, Carol REGISTRATION NUMBER: 3
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                                                                           TOPOLOGY:
                                                                                         TYPE: AMINO ACID
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
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US-08-742-774-8
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INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-496-847-8
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Matches 9; Conser
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                                            Patent No.
                                                          Sequence 8, Application US/08742774
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Best Local
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GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
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TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 8:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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MEDIUM TYPE: Diskette
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LENGTH: 26 amino acids
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STATE: CA
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350 Cambridge Avenue, Suite 250
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N: 514
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Pred. No. 0.31;
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Search completed: January 14, 2003, 18:32:23 Job time: 15 secs
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APPLICATION NUMBER: US/08/049,794
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
NAME: Stratford, Carol A.
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REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
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MEDIUM TYPE: Floppy
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ZIP: 94306
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CITY: Palo Alto
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                  1 CXIXNQXCXQXLDDCCSXXCNXXNXC 26
                                                                 CKLKGQSCRKTSYDCCSGSCGRSGKC
                                                                                                                                                                                                                                                                                               amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA
                                                                                                                                                                                                                                                                                                                                  26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Law Offices of Peter Dehlinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (415) 324-0880
                                                                                                                                                                                                                                                                NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                protein
                                                                                                                                                        64.2%;
                                                                                                                                                                                                                             SVIB/SNX-183, FIGURE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/742,774
                                                                                                                                                                                                                                                                                                                                                                        œ
                                                                                                                                     12;
                                                                                                                                                         Score 77;
Pred. No.
                                                                                                                                         Mismatches
                                                                                                                                                           0
                                                                                                                                                         DB 2;
0.31;
                                                                                                                                         <u>ن</u>
                                                                                                                                                                          Length 26;
                                                                                                                                           Indels
                                                                                                                                       0;
                                                                                                                                         Gaps
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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         January 14, 2003, 18:30:52; Search time 11 Seconds (without alignments)
47.621 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118974 seqs, 19401057 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            us-09-666-837B-1
120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Compugen Ltd.
                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                                                                                                  /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                                                                                                                                                                                /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_NRM_DUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

19	17	16	15	14	13	12	11	10	9	80	7	6	υ	4	ω	N	1	Result
63	2 6	63	63.5	63.5	63.5	63.5	63.5	63.5	64.5	64.5	64.5	65.5	65.5	65.5	66	66	68	Score
52.5	л () Э ()	52.5	52.9	52.9	52.9	52.9	52.9	52.9	53.8	53.8	53.8	54.6	54.6	54.6	55.0	55.0	56.7	Query Match I
1238	1212 550T	76	72	72	36	36	36	36	71	35	32	73	36	36	721	176	2444	Length I
10	1 5	و ب	10	10	10	10	10	10	10	10	10	10	10	10	10	9	10	B
US-09-855-722-5	US-09-855-722-3	US-09-749-637A-207	US-09-894-882-338	US-09-894-882-323	US-09-894-882-443	US-09-894-882-441	US-09-894-882-339	US-09-894-882-324	US-09-894-882-119	US-09-894-882-413	US-09-894-882-364	US-09-894-882-167	US-09-894-882-369	US-09-894-882-168	US-09-908-322-5	US-10-024-599-4	US-09-944-849-2	ID
5	Sequence 2, Appli	2 0	, 8	`	•	`	Sequence 339, App	Sequence 324, App	•	Sequence 413, App	Sequence 364, App	•	`	`	Sequence 5, Appli	Sequence 4, Appli	Sequence 2, Appli	Description

45	4.4	43	42	41	40	39	38	37	36	<u>3</u> 5	34	<u>ვ</u>	32	3 <u>1</u>	30	29	28	27	26	25	24	23	22	21	20
61	<u>ر</u> ع	61	61	61.5	61.5	61.5	61.5	61.5	61.5	61.5	62	62	62	62	62	62	62	62	62	62.5	62.5	62.5	62.5	62.5	63
50.8	50.8	50.8	50.8	51.2	51.2	51.2	51.2	51.2	51.2	51.2	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	52.1	52.1	52.1	52.1	52.1	52.5
3571	1480	1404	728	72	70	70	36	36	36	<u>3</u> 5	723	723	723	722	702	520	196	165	157	71	70	36	36	35	1238
9 1	12	10	10	10	10	10	10	10	9		10	10			10	10	10	10	10	10	10	10	10	10	10
US-10-150-821-2	US-10-011-064-5	US-09-944-849-8	US-09-908-322-2	US-09-894-882-107	US-09-894-882-206	US-09-894-882-200	US-09-894-882-403	US-09-894-882-401	US-09-814-452-25	US-09-894-882-409	US-09-995-593A-9	US-09-828-366-21	US-10-028-072-346	US-09-908-322-12	US-09-995-593A-4	US-09-995-593A-3	US-09-908-322-35	US-09-867-550-1550	US-09-908-322-68	US-09-894-882-74	US-09-894-882-209	US-09-894-882-404	US-09-894-882-210	US-09-894-882-433	US-09-944-849-4
,	Sequence 5, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 107, App	Sequence 206, App	Sequence 200, App	Sequence 403, App	Sequence 401, App	Sequence 25, Appl	Sequence 409, App	Sequence 9, Appli	Sequence 21, Appl	Sequence 346, App	Sequence 12, Appl	Sequence 4, Appli	Sequence 3, Appli	Sequence 35, Appl	Sequence 1550, Ap	Sequence 68, Appl	Sequence /4, Appl				Sequence 433, App	4,

## ALIGNMENTS

RESULT 1 US-09-944-849-2

Sequence 2, Application US/09944849 Patent No. US20020151487A1

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                                                                                                                                                             US-09-944-849-2
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APPLICANT: Nickoloff, Brian
APPLICANT: Miele, Lucio
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 2444
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/944,849
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 212583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREAT
                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1787)..(1787)
OTHER INFORMATION: The 'Xaa' at location
OTHER INFORMATION: Constitutively Active
                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1763)..(1763)
OTHER INFORMATION: The 'Xaa' at location 1763 stands for Gln, Arg, Pro, or Leu.
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (891)..(891)
OTHER INFORMATION: The 'xaa' at location 891 stands for Gly, or Ala
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
  248 GFTGQNCEENIDDCPGNNCKNGGACV 273
                                                                                                     Local
                                  2 XIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                Similarity 30.8
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-08-31
                                                                                                   56.7%;
                                                                                  12;
                                                                                                   Score 68;
Pred. No.
                                                                                    Mismatches
                                                                                                                                                                                     1787 stands for Thr, Ala, Pro, or Ser No. US20020151487A1ch-1
                                                                                                                      10; Length 2444;
                                                                                    Indels
                                                                                    0
                                                                                    Gaps
                                                                                    0;
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US-10-024-599-4

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RESULT 3
US-09-908-322-5
; Sequence 5, Application US/09908322
; Patent No. US20020107134A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENCTH: 176
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cimbora, Daniel M.
APPLICANT: Heichman, Karen
APPLICANT: Bartel, Paul L.
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 2318-278-II
CURRENT APPLICATION: """"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/024,599
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US 60/256,986
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: PEPTIDE
LOCATION: 1..176
OTHER INFORMATION: Xaa is Gly or Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity hes 8; Conserv
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                                                                          APPLICATION NUMBER: 08/981,392 FILING DATE: 22-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVCVNGWSGDDCSENIDDCAFASCTPGSTCI 39
                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                          CLASSIFICATION: <Unknown>
                   NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
                                                                                                                                                                                                                                                                                                                                                                                        STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
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                                                                                                                                                                                                                                                                                                                                             TRY: USA
10036/2711
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Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ish-Horowicz, David
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25.8%;
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Pred. No. 6
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6.6;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-908-322-5
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                                                                                                                                                                                                                                                                                                             SEQ ID NO 168
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-0 NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                      NAME/KEY: PEPTIDE LOCATION: (1)..(36)
LOCATION: (1)..(36)
OTHER INFORMATION: Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues OTHER INFORMATION: , 23 and 36 is Tyr, 1251-Tyr, mono-lodo-Tyr, di-lodo-Tyr, 0-su OTHER INFORMATION: o-Tyr or O-phospho-Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/264,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                            ORGANISM: Conus betulinus
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 GFSGRNCDDNLDDCTSFPCQNGGTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%;
Local Similarity 32.0%;
les 8; Conservat:...
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-11-14
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CLSLGQRCXRH-SDCCGXLCCFXDKCV 27
                               CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168, AF
                                                                    . Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Walker, Craig S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watkins, Maren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McIntosh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jimenez, Elsie C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shetty, Reshma
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                     version 3.0
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                                                                                    54.68;
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                                                                    ; Score 65.5; D
; Pred. No. 1.7;
9; Mismatches
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Pred. No. 24;
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Length 73;

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1;

Gaps

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CURRENT EILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/894,882
CURRENT EILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARED: DATESTANCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-894-882-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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US-09-894-882-369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0 SEQ ID NO 369
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 167, Application US/09894882 Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-894-882-167
                                                      TITLE OF INVENTION: I-Superfamily Conotoxi
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/9
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION UNWHER: US 50/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Utah Research Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CXIXNQXCXQXLDDCCSXXCNXXNXCV 27
                    APPLICATION NUMBER: US 60/246,581 FILING DATE: 2000-11-08
      APPLICATION NUMBER: US 60/247,714
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION
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Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. McChael
Olivera, Baldomero M.
Watkins, Maren
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9; Conservative
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                                                                                                                                                                                                                                               Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                                                                                                                                                                                                               Jones, Robert
Shen, Greg S.
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                                                                                                                                                                                                                                    Robert M.
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                                                                                                                                                                                             I-Superfamily Conotoxins
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33.3%; Pred. No. 1.
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CURRENT ETLING DATE: 2001-06-29
CURRENT ETLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR EPLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Conus betulinus US-09-894-882-167
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US-09-894-882-364
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                                                                                                 RESULT 8
US-09-894-882-413
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SOFTWARE: Pate
SEQ ID NO 364
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Best Local S
Matches 9
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Best Local Similarity 33.3%;
Matches 9; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 364, Patent No. US
Sequence 413, Application US/09894882 Patent No. US20020102607A1 GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR ETLING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US
PRIOR ETLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/264,256 PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc. APPLICANT: Walker, Craig S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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ENGTH: 73
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9; Conserv
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Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watkins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09894882
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                                                                                                                                                                                                                                                                        53.8%;
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Pred. No. 3.3;
                                                                                                                                                                                                                                                                        Score 64.5;
Pred. No. 1
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Length 32;

Indels

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Gaps

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Gaps

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APPLICANT: University of Utah Research Foundation
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetik, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Walker, Craig S.
APPLICANT: Walker, Craig S.
APPLICANT: Sheetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: Jimenez, Elsie C.
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: JONESE: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 119
LENGTH: 71
TYPE: DRT
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FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-10-30

PRIOR PRIOR PLICATION NUMBER: US 60/243,410

PRIOR PRIOR PLICATION NUMBER: US 60/244,410

PRIOR PRIOR PLICATION NUMBER: US 60/244,591

PRIOR PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-11-14

PRIOR FILING DATE: 2000-10-29

PRIOR FILING DATE: 2000-10-29

NUMBER OF SEQ ID NOS: 506

SOPTWARE: PATENT NUMBER: US 60/264,256

PRIOR APPLICATION NUMBER: US 60/264,256

PRIOR APPLICATION SUMBER: US 60/264,256

PRIOR APPLICATION SUMBER: US 60/264,256

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 506

SOPTWARE: PATENT NOS: 506

SOPTWARE: PATENT NOS: 506

SOPTWARE: PATENT NOS: 506

SEQ ID NO 413

LENGTH: 35
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US-09-894-882-119
; Sequence 119, Application US/09894882
; Patent No. US20020102607A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Conus magus
US-09-894-882-413
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Sup-
FILE REFERENCE: 2314-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 9; Conservat
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Shetty, Reshma
Jimenez, Elsie C.
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Olivera, Baldomero M.
Watkins, Maren
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33.3%; Pred. No. 2.1;
tive 11; Mismatches
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PRIOR APPLICATION NUMBER: US 60/2

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR APPLICATION NUMBER: US 60/245,410

PRIOR APPLICATION NUMBER: US 60/245,410

PRIOR APPLICATION NUMBER: US 60/247,714

PRIOR PRIOR FILING DATE: 2000-11-19

NUMBER OF SEC ID NOS: 506

SOFTWARE: PATENTIA PATENTIA VERSION 3.0

SEQ ID NO 324

LENGTH: 36

TYPE: PRI
ORGANISM: Conus episcopatus

FEATURE:
NAMEXEY: PEPFIUE

LOCATION: (1). (36)

OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro; Xaa at residue 23 is
OTHER INFORMATION: 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos

JUSCO JESS OF STATEMENT OF STAT
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US-09-894-882-324
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US~09-894-882-119
                                                                                                                                                                                                                                          RESULT 11
US-09-894-882-339
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APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
                                                                                                                                           GENERAL
                                                                                                                                                                       Sequence 339, Application US/09894882 Patent No. US20020102607A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 324, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.9%; Score 63.5;
Best Local Similarity 38.5%; Pred. No. 2
Matches 10; Conservative 9; Mismatch
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Walker, Reshma
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f: Shen, Greg S.
INVENTION: I-Sup.
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20020102607A1
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9; Mismatches י
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Query Match Best Local : Matches

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; LOCATION: (1)..(36)
; OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro
US-09-894-882-339
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PRIOR FILLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILLING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILLING DATE: 2001-01-29
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SEQ ID NO 339
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
                                                                            PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
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TYPE: PRT
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
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                     NUMBER OF SEQ ID NOS: 506
                                       PRIOR APPLICATION NUMBER: US 60/264,256 PRIOR FILING DATE: 2001-01-29
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PatentIn version 3.0
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McIntosh, J. Michael
Olivera, Baldomero M.
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Shen, Greg_S.
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Pred. No. 2
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Best Local
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Patent No.
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
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CURRENT FILING DATE: 2001-06-29
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
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TYPE: PRT
                                 APPLICANT:
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                                                                                                                           323, Application US/09894882
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9; Conserv
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chen, Greg S.
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Olivera, Baldomero M
Watkins, Maren
                                              Cognetix, Inc. Walker, Craig S. Shetty, Reshma
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              Jimenez, Elsie C.
McIntosh, J. Michael
Olivera,
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34.6%;
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Pred. No. 2
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APPLICANT

Watkins, Maren

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; LENGTH: 72
TYPE: PRT
; ORGANIEM: Conus episcopatus
US-09-894-882-338
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PPLICATION NUMBER: US 60/243,410
PRIOR PPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/246,714
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION DATE: 2001-01-29
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Best Local Similarity
"arches 9; Conservat
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; SEQ ID NO 323

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Conus episcopatus

US-09-894-882-323
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PRIOR FILING DATE: 2000-06-30
PRIOR PPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Shetty, Reshma
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 338
    Query Match 52.9%; Score 63.5; Best Local Similarity 34.6%; Pred. No. 4 Matches 9; Conservative 10; Mismatch
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TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
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34.6%; Pred. No. 4.9;
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                                              DB 10;
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                                            Length 72;
    Indels
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Job time : 12 secs
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Maximum Match 100%
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120
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

29	28	27	26	. 25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ъ	4	ω	2	_	Result No.
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51.7	51.7	51.7	52.5	52.5	52.5	53.3	53.3	53.3	54.2	54.2	54.2	54.2	54.2	54.2	55.0	55.0	55.0	55.0	55.8	55.8	55.8	55.8	55.8	56.7	57.5	60.0	64.2	100.0	Query Match Length
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A40136	I48324	A43620	T30176	A48836	S18174	T08618	T30201	T25933	T31070	S78549	S45306	T09059	D89711	T22025	A24420	A49128	A49175	B43620	A46019	S18188	S42612	A35672	в26637	A40043	<b>JH0699</b>	A35844	C44379	A58997	ID
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A; Title: A consensus

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49.2	49.2	49.2	50.0	50.0	50.0	50.0	50.0	50.0	50.8	50.8	50.8	50.8	50.8	50.8	51.2
43	43	25	1722	1295	880	833	832	354	1480	1469	1408	1025	728	29	36
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S33382	S18173	JH0701	E89753	A32901	S00670	S19087	A31246	T22274	A36665	в36665	S16148	T42626	150719	A58537	A32038
metallothionein -	metallothionein -	omega-conotoxin MV	protein F11C7.4 [1	glpl protein precu	neurogenic repetit	gene Delta protein	neurogenic protein	hypothetical prote	slit protein 1 pre	slit protein 2 pre	gene serrate prote	secreted leucine-r	C-Delta-l - chicke	omega-conotoxin MV	mu-agatoxin I - fu

### ALIGNMENTS

RESULT 1 A58997 A; Accession: C44379
A; Molecula C. C. C. A; Molecula C. C. C. A; Reference number: A44379; MOID: RESULT 2 C44379 R;Residues: 1-27 <TERN A;Residues: 1-27 <TERN C;Comment: This conotoxin blocks conductance of the Shaker potassium channel. C;Keywords: hydroxyproline; neurotoxin; venom C;Keywords: hydroxyproline (Pro) #status experimental R;Terlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M. Nature 381, 148-151, 1996
A;Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail. C;Species: Conus purpurascens (purple cone)
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999 kappa-conotoxin PVIIA - cone shell (Conus purpurascens)
N;Alternate names: fin-popping peptide C;Species: Conus striatus (striated cone)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Sep-2000
C;Accession: C44379 В 20 A; Molecule type: protein A; Residues: 1-27 <TER> A; Reference number: A58997 A; Accession: A58997 A; Note: sequence extracted from NCBI backbone (NCBIP:116002); structure R; Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J. submitted to the Brockhaven Protein Data Bank, August 1996 A; Molecule type: protein A; Residues: 1-26 < RAM> N; Alternate names: SNX-183 omega-conotoxin SVIB [validated] - cone shell (Conus striatus) A; Status: preliminary A;Contents: annotation; conformation by (1)H-NMR, residues 1-26 R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J. Mol. Biol. 263, 297-310, 1996 A; Experimental source: venom A; Cross-references: CAS:143306-19-8 A; Reference number: A67649; PDB:1MVJ Accession: A58997 Matches Best Query Match Local l Similarity 17; Conserv Zafaralla, G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, Conservative omega-conotoxins 9; MUID:93003172; 63.0%; 100.0%; Score 120; for omega-conotoxins with different selectivities 10; score 120; DB 2;
Pred. No. 4.3e-05;
0; Mismatches 0; from Conus striatus venom. PMID:1390774 Length 27; Indels 0; Gaps confirmed . .. 0; Gray, for ğ

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A;Title: Notch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
A;Accession: A35844
A;Status: preliminary; nucleic acid sequence not shown; not
A;Molecule type: mRNA
A;Residues: 1-2524 <COF>
C;Superfamily: notch protein; ankyrin repeat homology; EGF
C;Keywords: transmembrane protein
F;146-17/Domain: EGF homology <EGX1>
F;184-215/Domain: EGF homology <EGF2>
F;456-487/Domain: EGF homology <EGF3>
F;57-788/Domain: EGF homology <EGF3>
F;57-788/
                                                A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels. A;Reference number: JH0699; MUID:92337922; PMID:1352986
A;Recession: JH0699
A;Rocession: JH0699
A;Molecule type: mRNA
A;Residues: 1-29 <HIL>
A;Cross references: GB:540826; NID:9252126; PIDN:AAB22674.1; PID:9252127
A;Cross references: GB:540826; NID:9252126; PIDN:AAB22674.1; PID:9252127
A;Cross references: GB:540826; NID:9257126; PIDN:AAB22674.1; PID:9252127
A;Cross references: GB:540826; NID:9257126; PIDN:AAB22674.1; PID:9252127
A;Cross references: GB:540826; NID:9251296, PIDN:AAB22674.1; PID:9252127
A;Title: Solution structure of omega-conotoxin MVIIC determined by NMR.
A;Reference number: PC2380; MUID:95169113; PMID:7864862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omega-conotoxin MVIIC precursor [validated] - cone shell (Conus magus) (fragment) c;Species: Conus magus (magus cone) C;Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 15-Sep-2000 C;Accession: JH0699; PC2380 C;Accession: JH0699; PC2380 R;H111yard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran November 1997 Novemb
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A;Contents: annotation; conformation by (1)H-NMR
C;Comment: This omega-conotoxin blocks presynaptic calcium channels.
C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F;1-16,8-20,15-26/Disulfide bonds: #status predicted
F;26/Modified site: amidated carboxyl end (Cys) #status experimental
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F;1924-1956/Domain: ankyrin repeat homology
F;1957-1989/Domain: ankyrin repeat homology
F;1991-2023/Domain: ankyrin repeat homology
F;2024-2056/Domain: ankyrin repeat homology
F;2057-2089/Domain: ankyrin repeat homology
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Pred. No.
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <AN1>
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                                                                                                                     neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 16-Aug-1988 *sequence_revision 16-Aug-1988 *text_change 21-Jul-2000 C;Accession: B2663 C;Accession: B2667 R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; EMBO J. 6, 761-766, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
B26637
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A; Title: EGF homologous sequences encoded in the genome A; Reference number: A91081; MUID:87218537; PMID:3107986
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C;Superfamily: notch protein; ankyrin repeat he F;261-292/Domain: EGF homology <EGX1>F;494-525/Domain: EGF homology <EGX1>F;987-1018/Domain: EGF homology <EGX2>F;1149-1180/Domain: EGF homology <EGF5>F;1187-1218/Domain: EGF homology <EGF5>F;1187-1218/Domain: EGF homology <EGF5>F;1233-1264/Domain: EGF homology <EGF3>F;1233-1264/Domain: ankyrin repeat homology <AIF;1940-1992/Domain: ankyrin repeat homology <AIF;1940-1992/Domain: ankyrin repeat homology <AIF;1940-2056/Domain: ankyrin repeat homology <AIF;2027-2059/Domain: ankyrin repeat homology <AIF
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A;Contents: annotation; conformation by (1)H-NMR
C;Superfamily: omega-conotoxin
C;Superfamily: omega-conotoxin
C;Skoywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel
F;3-28/Product: omega-conotoxin MVIIC #status experimental <MAT>
F;3-18,10-22,17-28/Disulfide bonds: #status experimental
F;3-18 Modified site: amidated carboxyl end (Cys) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 3-28 <NEM>
R; Farr-Jones, S.; Basus, V.J.
submitted to the Brookhaven Protein Data Bank, December 1994
A; Reference number: A66297; PDB:10MN
A; Contents: annotation; conformation by (1)H-NMR, residues 3-28
A; Contents: annotation; J. L. Remachandran, J.
                                                                                                                                                                                           F;2027-2059/Domain: ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 66, 649-661, 1991
Cell 66, 649-661, 1991
A;Title: TAN-1, the human homolog of the Drosophila Notch
A;Title: TAN-1, the human homolog of the Drosophila Notch
A:Reference number: A40043; MUID:91347367; PMID:1831692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          notch protein homolog TAN-1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 02-Aug-2002
C;Accession: A40043
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A;Cross-references: GB:M73980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence
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                                                                                                                                        Query Match
Best Local
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Best Local
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248
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GFTGQNCEENIDDCPGNNCKNGGACV
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                                                                                                        Similarity
8; Conserv
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8; Conserv
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Pred. No. 2
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Pred. No.
273
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                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat homology;
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<AN5>
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of Drosophila melanogaster,

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A;Accession: B26637
A;Molecule type: mRNA
A;Residues: 1-293 <KNU>
A;Cross-references: GB:X05144; NID:g7519; PIDN:CAA28793.1; PID:g929536
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: transm
F; 139-170/Domain:
F; 177-208/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: FlyBas
C;Superfamily: unassigned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 11-Jan-2000
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                                                                                                                                                            transmembrane protein precursor - zebra fish C;Species: Brachydanio rerio (zebra fish) C;Date: 20-Feb-1995 #sequence_revision 20-Feb
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                                                                                                                                                                                                                                                                                                                                                                                                                F;691-722/Domain: E0
F;767-799/Domain: E0
F;1878-1914/Domain:
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F;392-424/Domain: EGF
F;691-722/Domain: EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: transmembrane
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A; Residues: 1-2139 <TEP>
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                                                              R;Bierkamp, C.; Campos-Ortega, J.A. Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic A;Reference number: S42612; MUID:94128602; PMID:8297791
A;Accession: S42612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: FlyBase: FBgn0000368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: FlyBase:crb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2437 <BIE>
A;Cross-references: EMBL
                                                                                                                                                C; Accession: S42612
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EGF homology <EGF>
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F homology <EGF>
 EMBL: X69088; NID: g433866; PIDN: CAA48831.1; PID: g433867
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28.0%;
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RESULT
S18188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Rattus norvegicus (Norway rat)
C; Date: 19-Feb-1994 #sequence_revision 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during
A;Reference number: S18188; MUID:92111383; PMID:1764995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   notch protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X57405; NID:g57634; C;Superfamily: notch protein; ankyrin repeat F;987-1018/Domain: EGF homology <EGF1>
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A; Molecule type: mRNA
A; Residues: 1-2531 <WEI>
 C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
C;Accession: A46019; S25144
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F;2050-2082/Domain: ankyrin repeat homology
                                                                                    A;Status: not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-2531 <DEL>
                                                                                                                                     A;Title: Cloning, analysis, and chromosomal localization A;Reference number: A46019; MUID:93194170; PMID:8449489 A;Accession: A46019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1984-2016/Domain:
                                                                                                                                                                                           R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Genomics 15, 259-264, 1993
                                                                                                                                                                                                                                                                                                      Notch-1 protein -
A; Description:
                                                                                                                                                                                                                                                                                   N;Alternate names: motch protein
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9; Conserv
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8; Conserv
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Expression pattern of Motch,
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30.8%;
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Pred. No.
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homology;
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 mouse homolog of Drosophila Notch, sugg
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F;144-175/Johnain: EGF homology <EGG12>
F;222-254/Domain: EGF homology <EGG72>
F;339-370/Johnain: EGF homology <EGG72>
F;339-370/Johnain: EGF homology <EGG33>
F;416-449/Johnain: EGF homology <EGG33>
F;416-449/Johnain: EGF homology <EGG3>
F;446-452/Johnain: EGF homology <EGG65>
F;456-480/Johnain: EGF homology <EGG65>
F;456-480/Johnain: EGF homology <EGG85>
F;532-563/Johnain: EGF homology <EGG95>
F;607-580/Johnain: EGF homology <EGG95>
F;795-882/Johnain: EGF homology <EGG95>
F;795-882/Johnain: EGF homology <EGG12>
F;795-826/Johnain: EGF homology <EGG12>
F;911-942/Johnain: EGF homology <EGG12>
F;911-942/Johnain: EGF homology <EGG13>
F;911-942/Johnain: EGF homology <EGG15>
F;1023-1056/Johnain: EGF homology <EGG15>
F;1149-1180/Johnain: EGF homology <EGG15>
F;1149-1180/Johnain: EGF homology <EGG17>
F;1149-1180/Johnain: EGF homology <EGG17>
F;1149-1180/Johnain: EGF homology <EGG17>
F;1135-1383/Johnain: EGF homology <EGG17>
F;1139-1425/Johnain: EGF homology <EGG19>
F;1139-1425/Johnain: EGF homology <EGG19>
F;1139-1425/Johnain: EGF homology <EGG19>
F;1194-1180/Johnain: EGF homology <EGG9>
F;1194-1180/Johnain: EGF homology <EGG19>
F;1194-1180/Johnain: EGF homology <EGG19>
F;1139-1425/Johnain: ankyrin repeat homology <AN1>
F;1917-1248/Johnain: ankyrin repeat homology <AN3>
F;2016-2048/Johnain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                     omega-conotoxin GVIIB - cone shell (Conus geographus)

# Alternate names: shaker peptide GVIIB

C;Species: Conus geographus (geography cone)

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 23-May-1997

C;Accession: B43620

# Colivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier,

Science 230, 138-1343, 1985

A;Title: Peptide neurotoxins from fish-hunting cone snails.

A; Reference number: A43620; MUID:86070213; PMID:4071055

A;Accession: B43620
                                                                                                                                                                                                                 C; Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline F;1-16,8-19,15-26/Disulfide bonds: #status predicted F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental
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A;Molecule type: mRNA
A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>
A;Cross-references: EMBL:Z11886
                                                                                                                                                                                                                                                                                                                  C; Superfamily: omega-conotoxin
                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-29 <OLI>
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F;144-175/Domain:
F;222-254/Domain:
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les 7; Conser
                                    1 CXIXNQXCXQXLDDCCSXXCNXXNXC
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region of chromosome
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
   55.0%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.8%; Score 67; 30.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                14; Mismatches
                                                                                                                           Score 66; DB 2; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6,
                                                                                                                                                         Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2531;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.; Rivier, J.;
                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                             Gaps
                                                                                             0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santo
                                                                                                             F:1029-106/Domain: EGF homology <EGF>
F:1067-1098/Domain: EGF homology <EGF3>
F:1153-1184/Domain: EGF homology <EGX3>
F:1191-1222/Domain: EGF homology <EGX4>
F:1876-1908/Domain: ankyrin repeat homology <AN1>
F:1909-1941/Domain: ankyrin repeat homology <AN2>
F:1943-1975/Domain: ankyrin repeat homology <AN3>
F:1976-2008/Domain: ankyrin repeat homology <AN3>
F:2009-2041/Domain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                     F;799-830/Domain: EGF homology <EGX1>
F;799-830/Domain: EGF homology <EGX1>
F;877-908/Domain: EGF homology <EGX2>
F;1029-1060/Domain: TGF homology <EGX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: Schwann cell
A; Note: sequence extracted from NCBI backbone (NCBIP:127811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Notch2: a second mammalian Notch gene. A; Reference number: A49128; MUID:93202015; PMID:1295745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell-fate determining gene Notch2 protein - rat C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: notch protein; ankyrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-2471 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A49128; A; Accession: A49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Weinmaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1203 <LAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development 116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Motch B protein
Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 8
                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roberts, V.J.; Lemke,
                          55.0%;
25.8%;
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В 20

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Pred. No. yo;
4; Mismatches Score 66;

5.

Indels

4.

Length 2471;

repeat homology; EGF homology

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F;560-591/Domain: EGF homology <EGF>
F;674-705/Domain: EGF homology <EGX2>
F;712-743/Domain: EGF homology <EGF3>
F;836-867/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A;Title: Motch A and Motch B--two mouse Notch homologues

A;Reference number: A49175; MUID:93178563; PMID:8440332

A;Accession: A49175
                                                                                                                                                                                                                                                                                                                                C;Superfamily: unassigned ankyrin repeat proteins; F;143-174/Domain: EGF homology <EGX1> F;482-513/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:126158)
A;Note: Sequence extracted from NCBI backbone (NCBIP:126158)
C;Comment: This protein is one of the neurogenic proteins controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C;Accession: A49175; PH1570; S32113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown
                                                     1 CXIXN----QXCXQXLDDCCSXXCNXXNXCV 27
CVCVNGWSGDDCSENIDDCAYASCTPGSTCI 37
                                                                                                             Conservative
                                                                                                                                                                                                                                             homology <EGX1>
homology <EGF1>
homology <EGF>
homology <EGX2>
homology <EGX2>
                                                                                                                                     55.0%;
25.8%;
                                                                                                          14; Mismatches
                                                                                                                                     Score 66;
Pred. No.
                                                                                                                                                                   DB 2;
                                                                                                                                                                   Length 1203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coexpressed in a wide variet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g287990
                                                                                                          4;
                                                                                                          Gaps
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R;Tautz, D.

R;Tautz, D.

Rucleic Acids Res. 17, 6463-6471, 1989

A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA male A;Reference number: S09358; MUID:89385974; PMID:2780284

A;Accession: S09358

A;Acc
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N;Alternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; NoLecule type: DNA
A; NoLecule type: DNA
A; Residues: 1-2703 <KID>
A; Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
A; Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1950-1982/Domain: ankyrin repeat homology <AN1>
F;1983-2015/Domain: ankyrin repeat homology <AN2>
F;1988-2004/Domain: transmembrane #status predicted <TMM3>
F;2017-2049/Domain: ankyrin repeat homology <AN3>
F;2050-20082/Domain: ankyrin repeat homology <AN4>
F;2050-20082/Domain: ankyrin repeat homology <AN5>
F;20538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1064-1095/Domain: EGF homology <EGF3>
F;1187-1218/Domain: EGF homology <EGX3>
F;1746-1762/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;297-328/Domain: EGF homology <EGX1>
F;530-561/Domain: EGF homology <EGF1>
F;568-599/Domain: EGF homology <EGF2
F;588-1019/Domain: EGF homology <EGX2>
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A;Map position: 8.96-9.36
A;Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: transmembrane #status predicted <TMMI>
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A; Accession: A05267
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A; Residues: 1-48, 'I',
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A;Accession: A24768
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A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
В
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                                                                                                                                                                                                                                                                              Matches
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822
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                                                                                                                                4 XNOXCXQXLDDCCSXXCNXXNXCV 27
TGQKCETNIDDCVTNPCGNGGTCI 845
                                                                                                                                                                                                                                                                       Similarity 7; Conserv
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                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                       55.0%; Score 66; 29.2%; Pred. No.
                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                     1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 2703;
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                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              0;
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submitted to the EMBL Data Library, February 1996 A;Reference number: Z19503 A;Accession: T22025
                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein r40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22025
                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-601 <WIL>
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                                                                                                                                                      A; Map position: X
                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                           A; Gene: CESP:F40E10.4
                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                              A; Experimental source: clone F40E10
                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
114 GFEGDYCEKNIDDCVNSKCENGGKCV 139
                                     2 XIXNOXCXQXLDDCCSXXCNXXNXCV 27
                                                                              Conservative
                                                                                              54.2%;
                                                                                13; Mismatches
                                                                                              Score 65;
Pred. No.
                                                                                              DB
46;
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                                                                                                                   Length 601;
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Search completed: January 14, 2003, 18:32:03 Job time : 18 secs

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 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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101.806 Million cell updates/sec
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   P46530 brachydanio
Q01705 mus musculu
Q07008 rattus norv
Q035516 mus musculu
Q04721 homo sapien
Q94W30 rattus norv
P07207 drosophila
P31695 mus musculu
Q9172 rattus norv
Q9un47 homo sapien
P27087 colinus vir
P49013 strongyloce
Q88671 rattus norv
Q88516 mus musculu
Q9nyj7 homo sapien
P27607 rattus norv
Q9y219 homo sapien
P37607 rattus norv
Q9y219 mus musculu
Q9nyj7 homo sapien
P37607 rattus norv
Q9y219 mus musculu
P05483 conus catus
P37677 rattus norv
Q61483 mus musculu
Q00548 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P21783 xenopus lae
P37300 conus magus
P46531 homo sapien
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49.2	49.2	49.2	49.2	49.2	50.0	50.0	50.0	50.8	50.8	50.8	51.2
63	53	53	43	25	1376	1295	833	1480	1408	29	36
Н	μ	H	μ	Н	_	μ	Н	-	1	Н	
MT_CHICK	CTL_NPVAC	CTL1_NPVOP	MTA_COLVI	CXOB_CONMA	CRBH_HUMAN	GLP1_CAEEL	DL_DROME	SLIT_DROME	SERR_DROME	CXOD_CONMA	TXM1_AGEAP
•		, -	• •		P822/9 nomo sapien	_		P24U14 drosophila	-	_	P11057 agelenopsis

### ALIGNMENTS

RP RA RT	RA RAT	RT RP RT RA	• ****
MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LYS-52; PHE-54; MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASP-59; SER-62; ARG-63; LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.  PubMed-10818087; PHE-68; ASN-69 AND LYS-70.  PubMed-10818087; Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey J., Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.;  "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt interaction with the shaker K+ channel.";  J. Biol. Chem. 275:24639-24644(2000).	ucture 5:1585-1597(19 UCTURE BY NMR. UCTURE BY NMR. UCTURE BY NMR. UCTURE BY NMR. Guenneugues narin P., Guenneugues naruse-dimensional structure-dimensional structure. assium channel-block. Chemistry 37:5407-54	"Rappa-conotoxin PVIIA is a peptide inhibiting the shaker of channel.",  J. Biol. Chem. 273:33-38(1998).  [2] SEQUENCE OF 46-72, AND SYNTHESIS. PubMed=12074021; Terlau H., Shon KJ., Grilley M.M., Stocker M., Stuehmer W., Olivera B.M.; Strategy for rapid immobilization of prey by a fish-hunting marine "Strategy for rapid immobilization of prey by a fish-hunting marine snail."; Nature 381:148-151(1996).  STRUCTURE BY NMR. TISSUE=Venom; MEDLINE=98104087; PubMed=9438859; Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J., Craik D.J.; Scanlon structure and proposed binding mechanism of a novel potassium channel toxin kappa-conotoxin PVIIA.";	ONPU  ONPU  STANDARD; PRT; 72 AA.  \$5633;  5-DEC-1998 (Rel. 37, Created)  5-JUN-2002 (Rel. 41, Last sequence update)  5-JUN-2002 (Rel. 41, Last annotation update)  appa-conotoxin PVIIA precursor (Fin-popping peptide).  appa-conotoxin PVIIA precursor (Fin-popping peptide).  onus purpurascens (Purple cone).  cukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;  ceggastropoda; Conoidea; Conidae; Conus.  (CBI_TaxID-41690;  1]  EQUENCE FROM N.A., AND SYNTHESIS.  EEQUENCE FROM N.A., AND SYNTHESIS.  Talker C.S., Grilley M.M., Watkins M., Hillyard D.R., Gray  livera B.M.;

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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed~10398696;
Terlau H., Bocca
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BLOCKADE OF SHAKER CHANNEL BY PVIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA."; Blophys, J. 82:3003-3011(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperactivity.

hyperactivity.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Expressed by the venom duct.

MASS SPECITROMETRY: MM-3268.4; METHOD-FAB.

SIMILARITY: BELONGS TO THE O-SUPERRAMILY OF CONOTOXINS.

CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asi 50, Leu-57 and Asp-59 gave very low yields upon folding, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potassium channels. The rat brain voltage-gated potassium channel protein Kv1.1 is resistant to this toxin, but the voltage-gated potassium channel protein Shaker (Drosophila) is sensitive. The interaction site between the Shaker channel and this toxin is within the $5-56 loop of the Shaker channel and this toxin is not induces hyperactivity, followed by continuous contraction and extension of major fins, without immobilization or death. Injection of this peptide together with the delta-conotoxin PVIA causes the sudden tetanus of prey (STOP) syndrome, which is a single, lethal "fin-pop" in envenomated fish. In mice, induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1AV3; 18-NOV-98.
1KCP; 14-OCT-98.
otoxin; Toxin; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiol. 114:125-140(1999)
                                           Signal
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30:528-536(2001).
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                                                                                                                                                                                                                                          R-A, K,Q: 100% REDUCTION OF TOXICITY.
1-A: 3-FOLD DECREASE OF TOXICITY.
P-A: 100% REDUCTION OF TOXICITY.
N-A: 100% REDUCTION OF TOXICITY.
Q-A: 13-FOLD DECREASE OF TOXICITY.
K-A,R: 100% REDUCTION OF TOXICITY.
F-A,M: 100% REDUCTION OF TOXICITY.
F-Y: 11-FOLD DECREASE OF TOXICITY.
Q-A: 3-FOLD DECREASE OF TOXICITY.
N-A: 3-FOLD DECREASE OF TOXICITY.
L-A: 100% REDUCTION OF TOXICITY.
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                                                                                                          A: 1.5-FOLD DECREASE OF TOXICITY.
A: 100% REDUCTION OF TOXICITY.
A: 1.5-FOLD DECREASE OF TOXICITY.
A: 3.5-FOLD DECREASE OF TOXICITY.
A: 1.2-FOLD DECREASE OF TOXICITY.
A: 5-FOLD DECREASE OF TOXICITY.
                                         17-FOLD DECREASE OF TOXICITY.
19-FOLD DECREASE OF TOXICITY.
117-FOLD DECREASE OF TOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of kappa-conotoxin-PVIIA with
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                                           SIGNAL
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                                                                                      Presynaptic Amidation; (
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01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNY-2002 (Rel. 41, Last annotation update)
15-UNY-2002 (Rel. 41, Last annotation update)
Conus striatus (Striated cone)
Eukaryota, Metazoa; Mollusca; Castropoda; Caenogastropoda;
Necgastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6493;
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles regulars a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97070382; PubMed=8913308;
Nielsen K.J., Thomas L., Lewigs R.J., Alewood P.F., Craik D.J.;
"A consensus structure for omega-conotoxins with different
selectivities for voltage-sensitive calcium channel subtypes:
comparison of MVIIA, SVIB and SNX-202.";
J. Mol. Biol. 263:297-310(1996)
J. Mol. Biol. 263:297-310(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=93003172; PubMed=1390774;
Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D. Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M. Cruz L.J.;
"Novel alpha- and omega-conotoxins from Conus striatus venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
STRUCTURE BY NMR.
MEDLINE-97070382;
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MEDLINE=20037955; PubMed=10573284;
Lu B.-S., Yu F., Zhao D., Huang P.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Novel alpha- and omega-conotoxins Biochemistry 31:9919-9926(1992).
                                                                                                         pfam; PF02950; Conotoxin; 1.
Presynaptic neurotoxin; Neurotoxin;
                                                                                                                                                                                                                            EMBL; AF146346; AAD31906.1;
                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and block voltage-sensitive calcium channels (VSCC). This toxin blocks N-, P-, and Q-type calcium channels.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 46-71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Conopeptides from Conus striatus and Conus textile by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                        3D-structure
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63.0%; Pred. N
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                      OMEGA-CONOTOXIN
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                                                                                                                                                                                                                                     NOTC_XEI P21783;
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Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.,
"Novel omega-conotoxins from Conus catus discriminate amon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calcium channel subtypes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conus catus (Cat cone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Omega-conotoxin CVIC
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Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
Amphibia; Batrachia; Anura; Mesobatr
                                                                                                                                                01-MAY-1991 (Rel. 18, 01-OCT-1996 (Rel. 34, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amidation.
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                                                                                                                  Neurogenic
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TISSUE SPECIFICITY: EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 275:35335-35344(2000).

FUNCTION: Omega-conotoxins act at presynaptic membranes, and block voltage-sensitive calcium channels (VSCC) (By similarity). This toxin blocks N-, P-, and Q-type calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY:
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                                                                                                                                                                                                                                                                XENLA
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                                                                                                                                                                                                                                                                   STANDARD;
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BY SIMILARITY.
BY SIMILARITY.
AMIDATION.
56EFC382335C4A8B C
         Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73;
Pred. No.
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                                          Craniata; Vertebrata;
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            Pipidae;
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                                                                                                                           protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                  THE TENENT PROPERTY OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00179; EGF_CA; 23.
SMART; SM00001; EGF_like; 1
SMART; SM00004; NL; 2.
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MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.,
"Xotch, the Xenonus harris"
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SUBCELLULAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN I
SIMILARITY: BELONGS TO THE NOTCH FAMILY.
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PS00022; EGF_1; 34.
PS01186; EGF_2; 29.
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MEDLINE-92337922; Pubmed-1352986;
Hillyard D.R., Monje V.D., Mintz I.M., Bean B.F.
Ramachandran J., Miljanich G.P., Azimi-Zoonooz
Cruz L.J., Imperial J.S., Olivera B.M.;
"A new Conus peptide ligand for mammalian presy
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  presynaptic Ca2+ channels.";
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                                      B.P., Nadasdi L.,
ooz A., McIntosh J.M.,
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Biochem, Biophys. Res. Commun.
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J. Mol. Biol. 248:106-124(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95248539; PubMed=7731037;
Farr-Jones S., Miljanich G.P., Nadasdi L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure-activity relationships of omega-conoto 14 loop splice hybrids at N and P/Q-type calcium J. Mol. Biol. 289:1405-1421(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10373375
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                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed.
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TISSUE SPECIFICITY: Expressed b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC). This toxin blocks N-type calcium channels as well as types of high-threshold voltage-gated calcium channels resistant to both dihydropyridines
                                                                                                                                                                                                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM EDUTOPEAN BIOINFORMATICS Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                    1CNN;
                                                                                                                                                                                                                                                                                                         JH0699;
                                                                CXIXNQXCXQXLDDCCSXXCNXXNXC 26
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                                                                                                                                    W
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Pred. No.
                                                                                                                                   HYDROXYLATION (PROBABLE).
AMIDATION (G-29 PROVIDE ANIDE GROUP).
Y->A; HIGH DECREASE IN BINDING.
AC7A68948474728A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŀ.,
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type calcium channels.";
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01-NOV-1995 (Rel. 32,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mammalia; Eutheria;
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Neurogenic locus notch homolog protein 1 precur
(Translocation-associated notch protein TAN-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gray G.E., Mann R.S., Mitsiadis E., Henriqu
Banks A., Leiman J., Ward D., Ish-Horowitz
"Human ligands of the Notch receptor.";
am. J. Pathol. 154:785-794(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION OF LIGANDS MEDLINE=99180765; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ellisen L.W., Bird of Smith S.D., Sklar J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-2444 FROM N.A. MEDLINE-91347367; PubMed=1831692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
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                                                              cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Table 1 (1997) of the Drosophila notch gene, Table 1 (1997) of the Drosophila notch gene, chromosomal translocations in T lymphoblastic neoplasms
  This SWISS-PROT ent
between the Swiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl Jaggedl and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May be important for normal lymphocyte function. In altered form, may contribute to transformation or progression in some T-cell neoplasms. Involved in the maturation of both cD4+ and CD8+ cells in the thymus (By similarity). SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                            from the membrane (By similarity).
PTM: Phosphorylated (By similarity)
DISEASE: Notchi truncation is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane proteolytical processing NICD is trans
                                                                                                                                                                                                                                                                     which is proteolytically cleaved by a furin-like convertase in the trans-golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNT-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain stem and lung. Also present in most adults found mainly in lymphoid tissues. PTM: Synthesized in the endoplasmic reticulum
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human notch 1 (hN1) cDNA sequence.";
(SEP-2000) to the EMBL/GenBank/DDBJ databases
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ry is copyright. It is Institute of Bioinforma
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Jht. It is produced through Bioinformatics and the El
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Piam; PF00008; EGF; 36.
Piam; PF00003; ank; 6.
Piam; PF00006; notch; 3.
SMART; SM00248; ANK; 5.
SMART; SM00019; EGF_L1ke; 13.
SMART; SM00001; EGF_L1ke; 13.
SMART; SM00004; MI; 2
PROSITE; PS50088; ANK_REPEAT; PROSITE; PS50018; ANK_REPEAT; PROSITE; PS00010; ASX_HYDROXYL
PROSITE; PS00010; ASX_HYDROXYL
PROSITE; PS001186; EGF_L; 34.
PROSITE; PS001186; EGF_L; 34.
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_II.
InterPro; IPR001801; Notch.
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     Bioinformatics Institute. There are no rest-
profit institutions as long as its content
EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 4.

EGF-LIKE 5. CALCIUM-BINDING

EGF-LIKE 6.

EGF-LIKE 7. CALCIUM-BINDING

EGF-LIKE 10.

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15-JUN-2002 (Rel. 41, Last annotation
Crumbs protein precursor (95F).
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EGF-LIKE 33,
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RC STRAIN-Oregon-R; TISSUE-Embryo; RX MEDLINE-90263104; PubMed-2344615; A Tepass U., Theres C., Knust E.; T "Crumbs encodes an EGF-like protein prosophila epithelial cells and requestion the collection of the c
                                                                                                                                SMART; SM0019; EGF_Like; 16.
SMART; SM00001; EGF_Like; 16.
SMART; SM00001; EGF_Like; 16.
SMART; SM00282; LamG; 3.
PROSITE; PS00010; ASX_HYDROXYL; 15.
PROSITE; PS00022; EGF_L; 26.
PROSITE; PS01186; EGF_2; 17.
PROSITE; PS01187; EGF_CA; 12.
R PROSITE; PS01187; EGF_CA; 12.
R PROSITE; PS01187; EGF_CA; 12.
R PROSITE; PS01187; EGF_CA; 12.
R PROSITE; PS01187; EGF_CA; 12.
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Vaessin H.
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between
the Euro
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EMBO J. 6:761-766(1987).

1- FUNCTION: MAY PLAY A ROLE IN THE DEVELOPMENT O
POSSIBLY FOR THE ESTABLISHMENT AND/OR MAINTENA
POLARITY. IT MAY ACT AS A SIGNAL.

1- SUBCELLULAR LOCATION: Type I membrane protein.

1- PTM: PHOSPHORYLATED IN THE CYTOPLASMIC DOMAINS.

1- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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Pfam; PF00054; laminin_G; 3.
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    DR Pfam; PF00066; notch; 3.
DR PRINTS; PR00010; EGFBLOOD.
TR PRINTS; PR01452; NOTCH.
TR SMART; SM00248; ANK; 5.
R SMART; SM00179; EGF_CA; 19.
R SMART; SM00001; EGF_Like; 16.
PROSTTT: PS5008A: ***
PROSTTT:
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PROSITE: PS50297; ANK_REP
PROSITE: PS502197; ANK_REP
PROSITE: PS000102; EGF_1;
PROSITE: PS00102; EGF_2;
PROSITE: PS01186; EGF_2;
PROSITE: PS01187; EGF_26;
PROSITE: PS01187; EGF_26;
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MEDLINE=94128602;
Bierkamp C., Campo
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SIMILARITY: BELONGS TO THE NOTCH FAMILY.
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STRGE: Expressed in all cells in pregastrulation stages. During gastrulation is differentially expressed, accumulating predominantly in the prechordal mesoderm and notochord. At the end of gastrulation, expressed along the anterior-posterior axis including the developing neural plate and differentiating mesoderm. Also present in the developing
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P00740;
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p; IPR000561; EGF-11ke.
p; IPR000742; EGF_2.
p; IPR00181; EGF_Ca.
p; IPR001438; EGF_II.
p; IPR001800; Notch.
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1EDM.
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ASX_HYDROXYL; 23.
EGF_1; 34.
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O11705; Q9Qw58; Q99JC2; Q06007; Q61905; Q9ROX7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A)
DE (mT14) (p300).
GN NOTCH1 OR MOTCH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryo;
RX MEDLINE=93194170; PubMed=8449489;
RA Franco del Amo F., Gendoron-Maguire M., Swiatek P.J., Jenkins N.A.,
RA Copeland N.G., Gridley T.;
RT homolog of Drosophila Notch.";
RI Genomics 15:259-264(1993).
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SEQUENCE OF 7
STRAIN-CD-1;
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                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF 1651-ARG-GLN-ARG-ARG-1654
MEDLINE-98318619; PubMed-9653148;
Logeat F., Bessia C., Brou C., LeBail O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1950-2201 FROM N.A. MEDLINE-98029496; PubMed-9384671; Messerle M., Follo M., Nehls M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=93048835; PubMed=1425352;
MEDLINE=93048835; PubMed=1425352;
MEDLINE=93048835; PubMed=1425352;
                                                                                                                                                 among mammalian Notch family members.";
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
                                                                                                                                                                            Mizutani T., Taniguchi Y., Aoki T., Hashimoto "Conservation of the biochemical mechanisms of
                                                                                                                                                                                                        MEDLINE-2.
                                                                                                                                                                                                                   POST-TRANSLATIONAL PROCESSING
                                                                                                                                                                                                                                                          proteolysis."
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                                                                                                                                                                                                                                                                                                   MEDLINE=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Dynamic changes in gene expression during mouse embryonic stem cells.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1950-2201 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee J.S., Ishimoto A., Yanagawa S.1
"Murine leukemia provirus-mediated
to induction of HES-1 in a mouse T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1659-1673 FROM N.A. MEDLINE=99364499; PubMed=10437788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lardelli M.,
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MEDLINE=93050801; PubMed=14
                                                                                                                                                                                                                                                                     "Murine notch homologs
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development, si
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                      FUNCTION: Functions as a receptor for membrane-bound ligands Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation. May be involved in mesoderm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lett.
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                                                                                                                                                                                                                                             Chem.
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               somite
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PubMed=8440332;
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Motch, a mouse homolog
               formation
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                             -I- SIMILARITY: BÉLONGS TO THE NOTCH FAI
-I- SIMILARITY: CONTAINS 36 EGF-LIKE DOI
-I- SIMILARITY: CONTAINS 3 LINVNOTCH REI
-I- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                           PTM: Phosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteolytical processing NICD is translocated to ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) produced by alternative splicing.
TISSUE SPECIFICITY: Highly expressed in the brain
                                                                                                                                                                                                                                                            notch-derived peptide containing the intracellular domain (NICD)
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SUBCELLULAR LOCATION:
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PRINTS; PRO1452; NOTCH.
SMART; SM00179; EGE\_CA;
SMART; SM00001, EGE\_lik
SMART; SM00004; NL; 2. Pfam; PF00023; ank; 7. Pfam; PF00066; notch; InterPro; IPR001881;
InterPro; IPR001438;
InterPro; IPR000800; PRINTS; PR00010; EGFBLOOD. MGI:97363; X68278; CA AJ238029; PF00008; EGF; P00740; X82562; CAA57909.1; ; PS50088; ANK\_REPEAT; 2.
; PS50297; ANK\_REP\_REGION; 1; PS00010; ASX\_HYDROXYL; 22.
; PS00022; EGF\_1; 34.
; PS01186; EGF\_2; 27.
; PS01187; EGF\_CA; 21. ; IPR000152; Asx\_hydroxyl. ; IPR000561; EGF-1ike. ; IPR000742; EGF\_2. ; IPR00181; EGF\_Ca. ; IPR001838; EGF\_II. ; IPR001830; Notch. IPR002110; ANK. Transcription 1EDM CAA48339.1; -. 9; CAB40733.1; -. AAK14898.1; CAA77941.1; -. ANK; 3. EGF\_CA; 23. EGF\_like; 11. Notch1 Repeat; regulation; Repeat; ANK 22. Activator; Difference repeat; EGF-like Differentiation;

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Matches
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Best Local
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Q07008;
Q1-NOV-1995
15-JUL-1999
15-JUN-2002
                                                                                                      TISSUE=Schwann cell;
MEDLINE=92111383; PubMed=1764995;
                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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    Tanigaki K.,
Honjo T.;
                   FUNCTION.
MEDLINE=21094508;
                                                                                       Weinmaster G., Roberts V. "A homolog of Drosophila
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                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                     Neurogenic
                                                                       Development 113:199-205(1991).
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               InterPro;
                                     InterPro;
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[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                       development."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Notch2: a
                                                                                                   European
                                                                                                                                                                                                                                                                     days
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MEDLINE=93202015; PubMed=1295745; Meinmaster G., Roberts V.J., Lemke
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                                                                                                                                                                                                                                                                                                                                                                                                                             Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I., "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent neural progenitor cells to an astroglial fate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21331789; PubMed=11438922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                    FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jagged2 and Deltal to regulate cell-fate determination Upon ligand activation through the released notch intracellular
SUBUNIT: Het
                                              apoptotic programs (By similarity). Acts instructively to control the cell fate determination of CNS multipotent progenitor cells, resulting in astroglial induction and neuron/oligodendrocyte
                                                                                                                                                                 domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              progenitor cells to 29:45-55(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G., Roberts V.J., Lemke second mammalian Notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116:931-941(1992).
                                                                                                                                                   of differentiation, proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G.;
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THE PROPERTY OF THE PROPERTY O

bonds (By similarity).
SUBCELLULAR LOCATION: Type SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a terminal fragment N(EC) which are probably linked by disul and a N-' disulfide

proteolytical processing NICD I membrane protein. is translocated ç Following the nucleus (Ву

and, in early postnatal central nervous system (CNS) germinal zones of the CNS. Found in both subventricular and ventricular germinal zones. DEVELOPMENTAL STAGE: In the embryo, highest levals comes. TISSUE SPECIFICITY: Expressed in the brain, 14 and decrease rapidly to much levels occur lower levels kidney and spleen in the

cleaved by presentiin dependent yamma-secretase to release notch-derived peptide containing the intracellular domain (from the membrane (By similarity).

PTM: Phosphorylated (By similarity).

SIMILARITY: BELONGS TO THE NOTCH FAMILY.

SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

SIMILARITY: CONTAINS 5 ANK REPEATS. which is proteolytically cleaved by a furin-like converged which is proteolytically cleaved by a furin-like converged which is proteolytically cleaved by a furin-like converged trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(EC). Following ligand binding, it is cleaved by TNT-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then notch extracellular truncation (NEXT). This fragment is then notch extracellular truncation (NEXT). Synthesized in the endoplasmic reticulum as an inactive form is proteolytically cleaved by a furin-like convertase in the s-Golgi network before it reaches the plasma membrane to yield s-Golgi network before the yield s-Golgi

EMBL; X57405; CAA40667.1; HSSP; P00740; 1EDM. modified and this statement SWISS-PROT entry is copyright. It is produced through a collaboration requires a IPR000152; IPR000561; IPR000742; IPR001881; IPR002110; email to license@isb-sib.ch) Bioinformatics Institute. license ormatics Institute. There are no rest institutions as long as its content atement is not removed. Usage by ar EGF\_2. Asx\_hydroxyl. EGF-like. agreement (See http://www.isb-sib.ch/announce, Ьy restrictions and for S

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SMART; SM00248; ANK
SMART; SM000179; EGF
SMART; SM00001; EGF
SMART; SM00004; NL;
PROSITE; PS50008; A
PROSITE; PS500297; A
PROSITE; PS00010; A
PROSITE; PS00022; E
PROSITE; PS011187; E
PROSITE; PS011187; E
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PRINTS; PRO0011;
PRINTS; PR01452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00066;
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IPR000800; Notch.
                                                                                                                                                                                                                                          983
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LO; EGFBLOOD.
L1; EGFLAMININ.
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EGF_CA;
EGF_like
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ANK_REP_REGION; 1.

ASX_HYDROXYL; 22.

EGF_1; 35.

EGF_2; 26.

EGF_CA; 21.
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NOTCH INTRACELLULAR DOMAIN NOTCH INTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 7.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

CALCIUM-BINDING

EGF-LIKE 12.

CALCIUM-BINDING

EGF-LIKE 13.

CALCIUM-BINDING

EGF-LIKE 14.

CALCIUM-BINDING

EGF-LIKE 15.

CALCIUM-BINDING

EGF-LIKE 16.

CALCIUM-BINDING

EGF-LIKE 17.

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EGF-LIKE 18.

CALCIUM-BINDING

EGF-LIKE 20.

CALCIUM-BINDING

EGF-LIKE 21.

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EGF-LIKE 23.

CALCIUM-BINDING

EGF-LIKE 24.

EGF-LIKE 25.

EGF-LIKE 26.

EGF-LIKE 26.

EGF-LIKE 27.

CALCIUM-BINDING

EGF-LIKE 26.

EGF-LIKE 30.

CALCIUM-BINDING

EGF-LIKE 31.

EGF-LIKE 32.

CALCIUM-BINDING

EGF-LIKE 33.

EGF-LIKE 34.

EGF-LIKE 33.

EGF-LIKE 34.

EGF-LIKE 33.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Activator; Differentiation;
repeat; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation.
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8, CALCIUM-BINDING
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Best Local
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MOUSE STANDARD; PRT; 24

NTC2_MOUSE STANDARD; PRT; 24

035516; 060941; Q06008;
15-JUN-2002 (Rel. 41, Last sequence up

15-JUN-2002 (Rel. 41, Last annotation
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                                                                                                                                                                                       Lardelli
"Motch A
                                                                                                                                                                                                                         SEQUENCE OF 316-1518 FROM N.A. STRAIN-C57BL/6 X CBA; TISSUE-Embryo: MEDLINE-93178563; PubMed-8440332;
                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6; TISSUE-Thymus;
Hamada Y., Higuchi M., Tsujimo
"Complete amino acid sequence
single copy of mouse Notch2 ge
submitted (JUL-1994) to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                      SEQUENCE OF 1765-2153 FROM N.A.
MEDLINE-97075110; PubMed-8917536;
MILDER L.A., Bigas A., Kopan R., Brashem-Stein C., Bernst
MARTLIN D.I.;
"Inhibition of granulocytic differentiation by mNotchl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTCH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 GFAGQNCEENVDDCPGNNCKNGGACV 273
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                                                                                                                                                                    ch A and Motch B-two mouse Notch variety of tissues.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 30.8
8; Conservative
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Metazoa; Chordata; C
mu+heria; Rodentia; ל
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                      Sci.
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                                                                                                                                                                                                                                                                                                  sequence and mutliform transcripts
Notch2 gene.";
to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                       Tsujimoto
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                        U.S.A.
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POLY -ALA.
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CLEAVAGE BY FURIN-LIKE PROTEASE (B SIMILARITY).
BY SIMILARITY.
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Pred. No. 20;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                        93:13014-13019(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
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RY Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., ....

RY Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Itanisma Of Signal transcriptional activation ligands of the released notch intracellular or domain (NICD) it forms a transcriptional activator complex with CCC domain (NICD) it forms a transcriptional activator complex with CCC RBP-J Kappa and activates genes of the enhancer of split locus.

CC RBP-J Kappa and activates genes of the enhancer of split locus.

CC Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in specification and/or differentiation.

CC postimplantation development, probably in some aspect of cell postimplantation and a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide of Subcellular Location. Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
                                                                       This SWI
         between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain
[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POST-TRANSLATIONAL PROCESSING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saxena M.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higuchi M., Kiyama H., Hayakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Development 126:3415-3424(1999).
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embryonic lethality.";
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                                                                                                                                                                                                                                                                                                     proteolytical processing NICD is translocate ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown) produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in the brain, neuroepithelia, somites, optic vesicles and
                                                            SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Res. Mol. Brain Res.
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                                              entry is copyright. iss Institute of Bioi
       a license
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of Notchl and
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     agreement
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                                              ght. It is produced through Bioinformatics and the EN
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    (See http://www.isb-sib
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PROSITE; PS50008; A
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Transmembrane; Glycoprotein; S:
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: EGF_CA; 22.
: EGF_like; 1
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ANK_REP_REGION
ASX_HYDROXYL;
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repeat; EGF-like domain;
l; Phosphorylation;
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004721; 09H240; 099734;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
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Blaumueller C.M., Mann R
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Mammalia; Eutheria;
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                                                       Artavanis-Tsakonas S.;
"Human homologs of a Drosophila en'
a novel family of nuclear proteins.
Nat. Genet. 2:119-127(1992).
 POST-TRANSLATIONAL MEDLINE-97386453; E
                                                                                                                                   Stifani
                                                                                                                                                 MEDLINE=93265135;
                                                                                                                                                                                         SEQUENCE OF 1810-2447
                                                                                                                                                                                                                                Submitted
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Correa R.G., Camargo
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TISSUE-Breast tumor;
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Neurogenic locus notch homolog protein 2 precursor
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Motazoa; Chordata;
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                                                                                                                                 S., Blaumueller C.M.,
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te determining NOTCH
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IDENTIFICATION OF LIGANDS MEDLINE=99180765; PubMed=Gray G.E., Mann R.S., Mit.
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                            use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gray G.E., Mann R.S., Mitsiadis E., Hen
Banks A., Leiman J., Ward D., Ish-Horow
Banks A., Leiman J., Word D.,
"Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(1999).
or send an email to license@isb-sib.ch)
                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                 PTM: Phosphorylated (By similarity).
SIMILARITY: BELONGS TO THE NOTCH FAMILY.
SIMILARITY: CONTAINS 35 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleu TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, skeletal muscle and liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination Upon ligand activation through the released notch intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                         trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Affects the implementation of differentiation, prolifera apoptotic programs (By similarity).

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and terminal fragment N(EC) which are probably linked by dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90:281-291(1997).
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                                (See http://www.isb-sib.
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PRINTS; PRODOLO; EGFBLOOD.
PRINTS; PRODOL1; EGFLAMININ.
SMART; SM00248; ANK; 4.
SMART; SM00179; EGF\_CA; 22.
SMART; SM00001; EGF\_Like; 12.
SMART; SM00004; NL; 2. InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; L; AF308601; AAA36377.2; AF315356; AAG37073.1; L; U77493; AAB19224.1; L; U77493; AAB19224.1; L; P00740; IEDM. 3W; HGNC:7882; NOTCH2. 600275; PF00008; EGF; PF00023; ank; PF00066; ); IPR000152; Asx\_hydroxyl.
| IPR000561; EGF\_11ke.
| IPR000742; EGF\_2.
| IPR00181; EGF\_Ca.
| IPR001438; EGF\_II. IPR002049; Laminin\_EGF IPR000800; Notch. IPR002110; notch; 2. . ნ ANK.

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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

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EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BINDING

EGF-LIKE 10.

EGF-LIKE 11.

CALCIUM-BINDING

EGF-LIKE 11.

CALCIUM-BINDING

EGF-LIKE 12.

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EGF-LIKE 13.

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EGF-LIKE 14.

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EGF-LIKE 15.

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EGF-LIKE 16.

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EGF-LIKE 17.

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EGF-LIKE 18.

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EGF-LIKE 35.

LIN/NOTCH 1.

LIN/NOTCH 1.

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BY 
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Matches
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Best Local
                                           J. Comp. Neurol. 436:167-181(2001).

J. Comp. Neurol. 436:167-181(2001).

J. Comp. Neurol. 436:167-181(2001).

Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation (By similarity).

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).

SUBCELIULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.

TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous ventricular germinal zones. Also found in the heart, liver and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rattus norvegicus (Ratus norvegicus); Eukaryota; Metazoa; (Mammalia; Eutheria; IMCBI_TaxID=10116;
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15-JUN-2002
15-JUN-2002
15-JUN-2002
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Irvin D.K., Zurcher S.D., Nguyen
"Expression patterns of Notchi, I
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"Notch2: a second mammalian Notch gene.";
Development 116:931-941(1992).
[2]
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                                                                                                                                                                                                                                                                                                                          development.";
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reticulum as a furin-like

an inactive convertase inactive

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EMBL; M93661; AAK13558.1; -.
HSSP; P00743; ICCF.
InterPro; IPR000151; AAK.
InterPro; IPR000152; Asx_hydro
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF-2.
InterPro; IPR001488; EGF_CI.
InterPro; IPR001881; EGF_CI.
InterPro; IPR001881; EGF_II.
InterPro; IPR002049; Laminin_B
InterPro; IPR002049; Laminin_B
Ffam; PF00008; EGF; 35.
Pfam; PF00008; EGF; 35.
Pfam; PF00008; notch; 2.
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Piam; PF00003; ank; 6.
Piam; PF00006; notch; 2.
Piam; PF00006; notch; 2.
PRINTS; PR00010; EGF1AMII
PRINTS; PR00111; EGF1AMII
PRINTS; PR000142; NOTCH.
SMART; SM00248; ANN; 4.
SMART; SM00179; EGF_CA; 3MART; SM000001; EGF_11ke.
SMART; SM000001; EGF_11ke.
SMART; SM000004; NL; 2.
PROSITE; PS50088; ANK_REI
PROSITE; PS50088; ANK_REI
PROSITE; PS00010; ASK_HYI
PROSITE; PS00010; ASK_HYI
PROSITE; PS0001186; EGF_2;
PROSITE; PS001186; EGF_CA
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from the membrane (By similarity).
PTM: Phosphorylated (By similarity).
SIMILARITY: BELONGS TO THE NOTCH FAMILY.
SIMILARITY: CONTAINS 35 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 LIN/NOTCH REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E; PS50068; ANK_REPEAT; 4.
E; PS50097; ANK_REP_REGION; 1
E; PS50097; ANK_REP_REGION; 1
E; PS00010; ASX_HYDROXYL; 22.
E; PS00022; EGF_1; 34.
E; PS01186; EGF_2; 26.
E; PS01187; EGF_CA; 22.
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an email to license@isb-sib.ch).
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Glycoprotein;
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1; EGFLAMININ.
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4; EGF_CA, 22.
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ASX. hydroxyl.

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Laminin_EGF.
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STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE-86079539; PubMed-3935325;
Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
"Nucleotide sequence from the neurogenic locus notch implies a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTC_DROME STANDARD: PRT; 2/U3 AA. P07207: P044154; 097458; Q9W4T8; 01-NOV-1986 (Rel. 03, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product that shares homology with
repeats.";
Cell 43:567-581(1985).
[2]
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Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brack
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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MEDLINE=20196011; PubMed=10731137;

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-i-FUNCTION: Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with Su(H).
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nelanogaster."
                                                                                                                                                                                             (Suppressor of hairless) and activates genes of the enhancer of split locus. Essential for proper differentiation of ectoderm. SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE NOTCH FAMILY. SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 31 LIQNOTCH REPEATS. SIMILARITY: CONTAINS ANK REPEATS.
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Pubmed=2981631;
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SMART; SM00191; EGF_CA;
SMART; SM00104; NL; 2.
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PROSITE; PS50008; ANK_RE
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L; M12175; AAA7449;
L; M16025; AAA2872;
; A24420; A24420;
; A24768; A24768.
; A05267; A05267.
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PF00023; ank; 6.
PF00066; notch; 3
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K03508;
M13689;
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PS01187;
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IPR000561; EGF-like.
IPR000742; EGF_2.
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in; Transmembrane; Glyco
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AAA28725
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5; CAB37610.1; JOINED
AAA74496.1; -.
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1; EGFLAMININ
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EGF; 36.
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; ANK_REP_REGION;
; ANK_REP_REGION;
; ASX_HYDROYL; 22
; EGF 1; 34 ...
; EGF 2; 28
; EGF 2; 28
; EGF_CA; 21
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; EGF_II.
; Laminin_EGF.
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    66;
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RESULT 15
NTC4_MOUSE
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OF VAL-1463
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NTC4_MOUSE STANDARD; PRT; 1964 AA. p31695; 062389; 062390; 035442; Q9R1W9; 088314; 01-JUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Neurogenic locus notch homolog protein 4 precurs (Contains: Transforming protein Int-3]. NOTCH4 OR INT3 OR INT-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasl Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., "Sequence of the mouse major histocompatibility locus class region.";
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gene in a mouse mammary tumor: generation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uyttendaele H., Marazzi G., Wu G., Yan Q "Notch4/int-3, a mammary proto-oncogene, cell-specific mammalian Notch gene.";
                                          MEDLINE=21523956; PubMed=11518718;
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"Vyttendaele H., Ho J., Rossant J., Kitajewski J.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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MEDLINE-96281668; PubMed-8681805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The mouse mammary tumor associated the NOTCH gene family (NOTCH4)."; Oncogene 14:1883-1890(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92194507; pubMed-1312643;
Robbins J., Blondel B.J., Gallahan D., Cal
"Mouse mammary tumor gene int-3: a member
transforms mammary epithelial cells.";
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Mammalia; Eutheria; Rodentia;
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                                                                                                                     98:5643-5648(2001).
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce,
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the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl Jaggedl and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May regulate branching morphogenesis in the developing vascular system.

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                      L; AF030001; AAB82004.1; AB016771; BAA32281.1; AB016772; BAA32283.1; AB016773; BAA32284.1; AB016774; BAA32285.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart kidney, and at lower levels in the ovary and skeletal muscle. A very low expression is seen in the brain, intestine, liver and
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SUBCELLULAR LOCATION: Type
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Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
                                                                                                                        P08709; 1BF9

;; IPR002110; ANK.
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;; IPR000561; EGF-like.
;; IPR000742; EGF_2.
;; IPR001881; EGF_Ca.
;; IPR001438; EGF_II.

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PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00001; EGF_CA; 11.
SMART; SM00001; EGF_CA; 15.
SMART; SM00004; NL; 2.
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PROSITE; PS50297; ANK_REP_REGION;
PROSITE; PS00010; ASX_HYDROXYL; 11
PROSITE; PS00022; EGF 1; 28.
PROSITE; PS01186; EGF 2; 21.
PROSITE; PS01187; EGF_CA; 9.
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348
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GCEENLDDCAAATCAPGSTCI
              XCXQXLDDCCSXXCNXXNXCV
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Search completed: January 14, 2003, 18:31:05 Job time : 13 secs

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Ol3149 fugu rubrip

O99m55 drosophila

O42374 brachydanio

O9nc90 strongyloce

O9nyd2 xenopus lae

O9w6e1 gallus gall

O20204 caenorhabdi

O16004 lytechinus

O25253 lucilia cup

O9vqa9 drosophila

P91526 caenorhabdi
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## ALIGNMENTS

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Q9IBG4 PRELIMINARY; PRT; 778 AA.

AD Q9IBG4; PROCESSED (TrEMBLEEL 15, Last sequence update)
DT 01-0CT-2000 (TrEMBLEEL 19, Last sequence update)
DT 01-DEC-2010 (TrEMBLEEL 19, Last sequence update)
DE Secretory protein containing EGF domain precursor.

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

CAMPhibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

OX NCBL_TEAXID=8355;

RY SEQUENCE FROM N.A.

RY SEQUENCE FROM N.A.

RY WEDLINE-20245325; PubMed-10781962;

RX WEDLINE-20245325; PRO00152; Asx.hydroxyl.

DR InterPro; IPR000183; Asx.hydroxyl.

DR InterPro; IPR00183; EGF_II.

DR InterPro; IPR00183; EGF_II.

DR InterPro; IPR00183; EGF_II.

DR InterPro; IPR00183; EGF_II.

DR InterPro; IPR001943; EGF_II.

DR InterPro; IPR001943; EGF_II.

DR InterPro; IPR00194; EdFININ.

DR PROSTTE; PR00011; EGFLAMINN.

DR SMART; SM00012; EGF_II.

DR SMART; SM00012; EGF_II.

DR SMART; SM00013; EGF_II.

DR SMART; SM00016; EGF_II.

DR PROSTTE; PS00116; EGF_II.

DR PROSTTE; PS01186; EGF_II.

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gulan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gulan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McLison C., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Stapleon M., Skupski M.P., Smith T.,
RA Reinert K., Remington K., Stapleon M., Skupski M.P., Smith T.,
RA Reinert K., Remington K., Stapleon M., Skupski M.P., Smith T.,
RA Wang Z.-Y. Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Yellsan S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao O., Zheng L.,
Ra Chebs R.A., Nixon G., Robin R., Nou S., Zhao O., Zheng L.,
Ra Chebs R., Zhong R., Nixon K., Nou S., Zhao
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Pterygota; Neoptera; Endopterygota;
                                                                                        "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Fruit fly).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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ota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2146
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1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT
Q9IAT6
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Best Local S
Matches 7
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PRINTS; PRODO11; EGFLAMINN.

SMART; SM00179; EGF_CA; 11.

SMART; SM00201; EGF_like; 16.

SMART; SM00282; LamG; 3.

PROSITE; PS00101; ASX_HYDROXYL; 16.

PROSITE; PS001186; EGF_1; 25.

PROSITE; PS01186; EGF_2; 17.

PROSITE; PS01187; EGF_CA; 13.

Calcium-binding; EGF-like domain; G:
SEQUENCE 2146 AA; 233570 MW; 8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1823
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and embryonic expression Mech. Dev. 90:119-123(2000).
EMBL; AF146429; AAF27299.1; -.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PS00122; EGF 1; UNKNOWN_8.
PROSITE; PS01186; EGF_2; EGF_2; EGF_2; EGF_2; EGF_CA; 2.
Calcium-binding; EGF-like domain; Glycoprosequence 664 AA; 72547 MW; 0AD6C34C857
                                                                                                                               PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO0011; EGFLAMININ.
SMART; SM00051; DSL; 1.
SMART; SM000179; EGF_CA; 4.
SMART; SM00001; EGF_like; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9IAT6;
01-OCT-2000
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pfam; PF00008; EGF; 26.
Pfam; PF00054; laminin_G; 3.
                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00740; 1EDM.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001774; DSL.
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                                                                                                                                                                                                                                            Pfam; PF01414; DSL; Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                             InterPro;
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IPR000152; ASX_hydr, IPR000561; EGF-like; IPR000742; EGF_2; IPR001881; EGF_Ca.; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                      ; IPR000561; IPR000742; IPR0001881; IPR001438; IPR001438; IPR002049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10585570;
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EGF_Ca.
                                                                                                                                                                                                                                                                                                             DSL.
EGF-like.
EGF_2.
EGF_Ca.
EGF_II.
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EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laminin_G.
                                                                                                                                                                                                                                                                                             Laminin_EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
19,
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
  in; Glycoprotein;
0AD6C34C8579116B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Hy 8E23B9E32B761115
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4.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the zebrafish.";
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RESULT OPERATOR OF THE PROPERTY OF THE PROPERT
          RESULT 5
Q9NGV4
ID Q9NGV4
AC Q9NGV4;
DT 01-0CT-2000
DT 01-0CT-2000
DT 01-JUN-2002
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Best Local (
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Best I
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Q91902;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001774; DSL.
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[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A., Lewis J.,
"Expression of a Delta homologue in prospective neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L42229; AAC38017.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Drosophila neurogenic gene Delta.";
Nature 375:761-766(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chitnis A., Henrique D.,
                                                                                                                                                           436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chitnis A., Henrique D., Lewis J., Primary neurogenesis in Xenopus en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=95319503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chick."
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8; Conserv
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IPR001881;
IPR001438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000561;
        (TrEMBLiel.) (TrEMBLiel.) (TrEMBLiel.)
                                                                        PRELIMINARY
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=7596407;
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EGF_Ca.
EGF_II.
                                                                                                                                                                                                                                        55.0%;
32.0%;
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30.8%;
          15,
15,
21,
      , Created)
, Last sequence up
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Last sequence update)
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                                                                                                                                                                                                                                        Score 66;
Pred. No.
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                        26
                                                                                                                                                                                                                       Mismatches
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1.9;
                                                                                                                                                                                                                                                      DB 13;
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                      update)
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                                                                                                                                                                                                                                                                                       Repeat.
                                                                                                                                                                                                                                                      Length 721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kintner C.;
by a homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ish-Horowicz
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0010; EGFBLOOD.

PRINTS; PRO0011; EGFLAMIXIN.

SMART; SM00179; EGF_CA; 6.

SMART; SM00101; EGF like; 9.

SMART; SM00192; LDIA; 1.

SMART; SM00192; EGF_1; UNKNOW PROSITE; PS00100; ASX_HYDROXYL; UNKNOW PROSITE; PS001186; EGF_1; UNKNOWN_15.

PROSITE; PS01186; EGF_CA; 5.

Calcium-binding; EGF-like domain; Glyc SEQUENCE 1551 AA; 167816 MW; A97EJ
"Structure of Fugu Notch gene Submitted (JUN-1997) to the E EMBL; AB004829; BAA20535.1; HSSP; P00740; IEDM.
InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001743; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR002449; Hyalin.
InterPro; IPR002499; Laminin_EGF.
InterPro; IPR0021791; Laminin_G.
InterPro; IPR0021791; LDL_recept_A.
                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Notch 2 (Fragment).

Notch 2 (Fragment).

Fugu rubripes (Japanese pufferfish) (Takifugu rubripe Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodc
                                                                                                                                                                                                                                                                                                                 013149;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=31033;
                                                                                                                                                                  Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM .....
TISSUE-ENDOPLASMIC RETICULUM;
Donal eton J.D., Rubin G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2000) to the EMBL/GenBank/DDBJ EMBL; AF239608; AAF63500.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SP1070.
SP1070 OR CG9138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0031879; SP1070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *A reverse genetic screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                               278 TGKNCQHTIDDCASNPCQHGATCV
                                                                                                                                                                                                                                                                                                                                                                                                                                               4 XNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF02494; HYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                              Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%;
33.3%;
Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.D., Feen for
                                                                                                                                                                                                                          pufferfish) (Takifugu rubripes)
                                                                                 gene.
                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB Pred. No. 4.1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN_9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; Re
A97EA229E9384F31
                                                                                                                                                                                                                                                                                                                              2447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ن</u>
                                                                                                                                                                              Tetraodontiformes;
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                                                              databases
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InterPro;

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Best L
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                                                                                                                                                                                                                                                                                                                                        O9VM55 PRELIMINARX;
O9VM55;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 21, Last annotation update)
CG9138 protein.
SP1070 OR CG9138.
SP1070 OR CG9138.
SP1070 OR CG9138.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pterygota; Neotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pterygota; Neotera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Proceedings of the process of the proces
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PRINTS; PRO0011; I
PRINTS; PR00012; I
SMART; SM00248; AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
Pfam;
           Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., BrottLer P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferriars S., Fleischmann W.,
Fooler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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SMART;
SMART;
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InterPro;
                                                                                                                                                                   PROSITE; PS50088; ANK_REPEAT; 8.
PROSITE; PS50297; ANK_REP_REGION; 2.
PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS00022; EGF_1; UNKNOWN_35.
PROSITE; PS01186; EGF_2; 29.
PROSITE; PS01187; EGF_CA; 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
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                                                                                                                                                                                                                                                                                  MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                     STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydroxylation; Repeat
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279
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 A., Gong F.,
N.L., Harvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00004;
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_CA; 20.
EGF_like; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANK; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGFBLOOD.
EGFLAMININ.
                                                                                                                                                                                                                                                                                  PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like.
EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laminin_EGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.0%;
29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262541 MW; 1A8E2A372A085D84 CRC64;
 Heiman T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 6
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   Hernandez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
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                                                                                                                                                                                          G.L.G.,
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Best Local
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SMART; SM00032; CCP; 8.
SMART; SM00042; CUB; 3.
SMART; SM00179; EGFF_CA; 8.
SMART; SM00179; EGF_Like; 9.
SMART; SM00231; FA58C; 2.
SMART; SM00282; LAMG; 1.
SMART; SM00282; LAMG; 1.
SMART; SM00288; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Pallazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walllams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Weinstock G.M., Zhang G., Zhao Q.A., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Glibbs R.A., Myers E.M., Rubin G.M., Venter J.C., "The Control of the Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
PROSITE;
PROSITE;
PROSITE;
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InterPro;
InterPro;
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InterPro;
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InterPro;
InterPro;
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    2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001421; FA58_C.
InterPro; IPR001092; HLH_basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0031879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                4 XNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; pF00431; CUB;
pF000008; EGF;
pF00754; F5_F8;
pF002494; HYR;
pF00057; ldl_r;
pF00084; sushi
    TGKNCQHTIDDCASNPCQHGATCV
                                                                                                                                                                                                                                                                                                                                                                                                   3; PS00010; ASX_HYDROXYL; 11.
2; PS01180; CUB; 6.
3; PS01012; EGF_1; 15.
4; PS01186; EGF_2; 13.
5; PS01187; EGF_CA; 7.
6; PS01285; FA58C_1; 1.
6; PS01208; LDLRA_1; 1.
7; PS01209; LDLRA_2; 2.
8; PS50068; LDLRA_2; 2.
8; PS50068; EGF-1ike domain; Glimpiding; EGF-1ike domain; EGF-1ik
                                                                                                                                                                               Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000152; Asx_hydroxyl.
IPR000859; CUB_domain.
IPR000561; EGF-like.
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IPR001791; Laminin_G.
IPR002172; LDL_recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houston K.A., Howland T.J., Wei M.-H.,
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ldl_recept_a;
sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _F8_type_C;
                                                                                                                                                                                                                         33.3%;
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                                                                                                                                                                                                                                                                                                                                                                       369389 MW;
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                                                                                                                                                       Pred. No. o..,
ll; Mismatches
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                                                                                                                                                                                                                                                                        Score
                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Hydroxylation; E618E9ACEA13E0E5 CRC64;
                                                                                                                                                                                                                         No :
                                                                                                                                                                                                                    DВ
3.3;
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                                                                                                                                                                                                                                                                    Length 3396;
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Lin X.,
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Best Local S
Matches 8
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PRINTS; PRO0011; E
PRINTS; PRO0011; E
SMART; SM00101; EC
SMART; SM00001; EC
SMART; SM00004; N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Scavenger receptor cysteine-rich protein variant 1.
Strongylocentrotus purpuratus (Purple sea urchin)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea; Etechinoidea; Strongylocentrotus purpuratus (Purple sea urchin)
                                                                                                                                                                                                                                                          Q9NC90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  042374
042374;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                 Strongylocentrotus NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00010; ASX_HYDROXYL; 9.
PROSITE; PS00022; EGF_1; UNKNOWN_1
PROSITE; PS01186; EGF_2; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Westin J., Lardelli M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
      SEQUENCE FROM N.A. MEDLINE=20542095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calcium-binding; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                          132
                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                             XNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                     SGDNCQTHIDDCSSNPCRNGGTCV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene evolution and function 
Genes Evol. 207:51-63(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y10354; CAA71380.1;
P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000152; / IPR000561; I IPR000742; I IPR001881; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001438;
IPR000083;
                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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TremBLrel. 05, Last se
TremBLrel. 20, Last an
r protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notch;
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      PubMed=11069281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF_CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          752
82103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     like; 5.
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function.";
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Pred.
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30939E16E0327F8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
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                                                                                                                                                                                                                                                                                1075
                                                                                                     Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
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                                                                                                                               Echinozoa;
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    DORREST DE RATE DE RAT
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01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
PROSITE;
PROSITE;
EGF-like
  PROSITE;
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PROSITE;
PROSITE;
                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-SERRATE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-serrate-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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PS00010;
PS00022;
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PRINTS; PRO0010; EGFBLOOD.
PRINTS; PR00258; SPERACTRCPTR
SMART; SM00032; CCP; 1.
SMART; SM00179; EGF_CA; 2.
SMART; SM00001; EGF_like; 1.
SMART; SM00202; SR; 6.
                               InterPro; IPR000561; E
InterPro; IPR000742; E
InterPro; IPR001881; E
InterPro; IPR001007; V
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; InterPro; IPR000561; InterPro; IPR000742; InterPro; IPR000742; InterPro; IPR001881; InterPro; IPR001881; I
                                                                                                                                                                                               "X-Serrate-1 is involved in primary neurogenesis in a complementary manner with X-Delta-1.";
                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Eukaryota; Mctazoa; Chordata; Craniat
Amphibia; Batrachia; Anura; Mesobatra
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00530; SRCR; 7. Pfam; PF00084; sushi; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pancer Z.;
"Dynamic expression of in coelomocytes of the
                                                                                                                                                                                                                                                MEDLINE=21541033; PubMed=11685570;
Kiyota T., Jono H., Kuriyama S., H
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF228824;
HSSP; P00740; 11
                                                                             InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001774; DSL.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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InterPro; IPR001190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 XNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                  Genes Evol. 211:367-376(2001).; AB027537; BAB59049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGSSCDTEIDDCSSSPCGDNGVCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00008; EGF; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PS00010; ASX_HYDROXYL; UNKNO
; PS00022; EGF_1; UNKNOWN_2.
; PS01186; EGF_2; 3.
; PS01187; EGF_CA; UNKNOWN_1.
; PS00420; SRCR_1; UNKNOWN_3.
; PS50287; SRCR_2; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1075 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF76316.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Receptor.
AA; 116178 MW; 61395AD6FD30BA3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPERACTROPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i52; Asx_hydroxyl.
i61; EGF-like.
ASX_HYDROXYL; UNKI
EGF_1; UNKNOWN_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                    14.
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                                                                 VWF_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Srcr_receptor.
Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple scavenger receptor purple sea urchin."; U.S.A. 97:13156-13161(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                   19,
19,
21,
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                                                                                                                                                                                                                                                                                                                                                Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                   Craniata;
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                 UNKNOWN_10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNKNOWN_2.
                                                                                                                                                                                                                                                 Hasegawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1214
                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                  Pipoidea;
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                                                                                                                                                                                                                                                 Miyatani S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6,
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                                                                                                                                                                                                                 Xenopus
                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Pipidae;
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Q9W6E1
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SQ
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Best I
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Best Local
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                                                                                                                                                                                                                                                                                                 PRINTS; PRO0010; EGFBLOOD.
ProDom; PD000918; Link; 2.
SMART; SM00003; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00019; EGF_CA; 1.
SMART; SM00001; EGF_Like; 1.
SMART; SM00001; EGF_Like; 1.
SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
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SMART; SH
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 1g; 1.
Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chondroitin Sulfate Proteoglycan Neurocan.";
J. Cell Biol. 149:1275-1288(2000).
EMBL; AF118856; AAD24546.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TIEMBLIEL 12, 01-NOV-1999 (TIEMBLIEL 12, 01-JUN-2002 (TIEMBLIEL 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20309833; PubMed-10851024;
Li H., Leung T.C., Hoffman S., Balsamo J., Lilic
"Coordinate Regulation of Cadherin and Integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurocan core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9W6E1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P08709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                      Match
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          XIXNQXCXQXLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conserv
                                               Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01186; EG
PS01187; EG
1214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; IPR000152; Asx_hydroxyl.
; IPR000561; EGF-like.
; IPR000742; EGF_2.
; IPR001881; EGF_Ca.
; IPR001438; EGF_II.
                                                                                                                                                                                                                                            PS00010; ASX_HYDROXYL; UNKNO
PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001304;
IPR000538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001881;
IPR001438;
IPR003599;
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                                                                                                                             Ã,
                                                                                                                           EGF-like domain; Glycoprotein; Repeat.
AA; 138877 MW; 182BD86D0E40BE78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGF_2; UNKNOWN_12.
EGF_CA; UNKNOWN_8.
A; 133807 MW; A9C
                                                                                                                                                                      LINK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Eute:
Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig.
Ig_MHC.
Lectin_C.
                                                               54.2%;
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26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sushi_SCR_CCP.
                                                                                                                                                                                                                             UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
                                               Score 65; DB
Pred. No. 4.7;
l3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred. No.
                                                                                                                                                                                                                                                                                       UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A9C09C420CC157C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
4.4;
                                                                   DB
4.7,
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egrin Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                               6;
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'
                                                                                    Length 1290;
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                                               Indels
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                                               Gaps
                                             0
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SMART; SMOUDS; LRRC1,

& SMART; SMOUDS; LRRC1,

AR SMART; SMOUDS; LRRTY; 4.

AR SMART; SMOUDS; LRRTY; 7.

AR SMART; SMOUDS; LRR_TYP; 7.

BR PROSITE; PSOUDO10, ASX_HYDROXYL; UNKNOWN_1.

DR PROSITE; PSOUDO22; EGF 1; UNKNOWN_7.

DR PROSITE; PSOUDS; EGF 2; 5.

DR PROSITE; PSOUDS; EGF_CA; 1.

DR PROSITE; PSOUDS; EGF_LA; 1.

PROSITE; PSOUDS; EGF_LA; 0.

PROSITE; PSOUDS; EGF-LIKe domain; Glycoprovation—binding; EGF-Like domain; Glycoprovation—binding
                                             A LO CONTROL DE LA RESTRICIO D
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Q20204
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                                                                                                                                                                                                                                          SMART; SM00041; C
SMART; SM00179; E
SMART; SM00001; E
SMART; SM00282; E
SMART; SM00370; E
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01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0010; EGFBLOOD. PRINTS; PRO0019; LEURICHRPT
                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                          Piam;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                           PF00054;
PF00560;
                                                                                                                                                                                                                                                                                                                                                                                      PF01462;
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                                                                                                                                                                                                                                                                                                                                                                                                      PF01463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z69792; CAB63434.1; JOINED
                                                                                                                                                                                                                                                                                                                                          PR00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000561;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    LRRCT; 4.
LRRNT; 4.
                                                                                                                                                                                                                                          ; CT; 1.
; EGF_CA; 2.
; EGF_like; 5.
; LamG; 1.
; LRR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                           LRR; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                             laminin_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_2.
EGF_Ca.
EGF_II.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRR_typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cys_knot.
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRR_out.
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21,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                           ; Glycoprotein; Repeat. 
0B5D198645D73670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.elegans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1440
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    Length 1440;
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J.L.,

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Query Match
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Matches 8
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Matches
                                                                                                                                                                                                                                                                                                                                       PRINTS; PROU415; ANKYRIN.
PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00179; EGF_CA; 23.
SMART; SM00001; EGF_like; 11.
SMART; SM00004; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     016004;
01-JAN-1998
01-JAN-1998
01-DEC-2001
  Q25253 PRELIMINARY;
Q25253;
Q1-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97454256; PubMed=9310331;
Sherwood D.R., McClay D.R.;
Sherwood D.R. and localization of
"Identification and localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            016004
                                                                                                                                                                                                                                  Hydroxylation;
                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development 124:3363-3374(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Notch homolog.
                                                                                                                                                                                                                                            ANK repeat; Calcium-binding;
                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification and localization of a sea urchin Notch homologing into vegetal plate regionalization and Notch receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytechinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
                                                                                                              661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                Local Similarity es 8; Conserv
                                                                                                                                    7 XCXQXLDDCCSXXCNXXNXCV 27
                                                                                                             NCEEDIDDCESRPCHNGGTCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFEGDYCEKNIDDCVNSKCENGGKCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00023; ank; 6.
PF00008; EGF; 35.
PF00066; notch; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF000634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                     PS50088; ANK_REPEAT; 10.
PS50297; ANK_REP_REGION; 2.
PS00010; ASX_HYDROXYL; 21.
PS00022; EGF_1; UNKNOWN_33.
PS01186; EGE_2; 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IPR000152; Asx_hydroxyl.
; IPR000561; EGF-1ike.
; IPR000742; EGF_2.
; IPR001841; EGF_Ga.
; IPR001438; EGF_II.
; IPR000800; Notch.
                                                                                                                                                                                                                                                           PS01187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002110; ANK.
                                                                                                                                                                                                                    2531 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrembLrel. 05, Created)
(TrembLrel. 05, Last seq
(TrembLrel. 19, Last ann
                                                                                                                                                                Conservative
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                  Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82088.1;
                                                                                                                                                                                                                                                          EGF_CA;
                                                                                                                                                                             54.2%;
38.1%;
                                                                                                                                                                                                                    273982 MW;
  01,
                                                                                                                                                                                                                            20.
ng; EGF-like domain; Glycoprotein;
                                                                                                              681
                                                                                                                                                             11;
  Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                             Pred.
                                                                                                                                                                                        Score 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                   5BF42BEC627CA303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                             No.
                                            2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2531 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G
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                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                        Length 2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notch homologue:
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxopneustidae;
                                                                                                                                                             0;
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                                                                                                                                                               Gaps
                                                                                                                                                             0;
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RESULT 15
Q9VQA9
ID Q9VQA
AC Q9VQA
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Best Local
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                        PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 4.
SMART; SM00179; EGF_CA; 24.
SMART; SM00001; EGF_like; 11.
SMART; SM00004; NL; 2.
Q9VQA9
Q9VQA9;
                                                                                                                                                                                                     PROSITE; PS50088; ANK REPEAT; 5.
PROSITE; PS50297; ANK REP_REGION; 1.
PROSITE; PS00297; ANK_REP_REGION; 1.
PROSITE; PS00012; ASK_HYDROXYL; 22.
PROSITE; PS00022; EGF_1; UNKNOWN_34.
PROSITE; PS01186; EGF_2; 28.
PROSITE; PS01187; EGF_CA; 21.
ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
                                                                                                                                                                                    Hydroxylation; Repeat. SEQUENCE 2653 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00066; notch;
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00023; ank; 6. Pfam; PF00008; EGF; 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF032670; AAC36152.1; JOINED EMBL; AF032671; AAC36152.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen Z., McKenzie J.A., Batterham Submitted (NOV-1997) to the EMBL/C EMBL, U58977; AAC36151.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen Z., Newsome T., Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McKenzie J.A., Batterham P.;
"Scalloped wings is the Lucilia cuprina Notch homologue and a
candidate for the modifier of fitness and asymmetry of diazinon
resistance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davies A.G., Game A.Y., Chen Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SS SEEKING;
MEDLINE-96400928; PubMed-8807304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Notch homolog scalloped wings (SCL).
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00740; 1EDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF032673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 39-265 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 39-265 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                              268 QGKNCEQNIDDCPGHLCQNGGTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
                                                                                                                                               Local
                                                                                                        4 XNQXCXQXLDDCCSXXCNXXNXCV 27
                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143:1321-1337(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000152;
IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEEKING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEEKING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002110; ANK.
                                                                                                                                   Conservative
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC36153.1;
                                                                                                                                             54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McKenzie J.A., Batterham to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                 Notch.
                                                                                                                                                                                     285928 MW;
                                                                                                                                12;
                                                                                                                                                           Score 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                              Pred.
                                                                               291
             PRT;
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams T.J.,
                                                                                                                                                                                     6AF2A058FEEC6329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.;
                                                                                                                                               No. 8
             838
                                                                                                                                                           DB 5;
             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                           Length 2653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodall S., Yen
                                                                                                                                 Indels
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RESULT Q25253 ID Q2 AC Q2 DT 01 DT 01

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В Š

0;

Gaps

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Mcilson D.R., Malson K.A., Nixon K., Nuzskern D.R., Pacleb J.M.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Worlis J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R., Nusskern D.R., Pacleb J.M.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Wand Z.-Y., Wassarman D.A., Weinstock G.M., Weinschach J.,

RA Wand Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
                                        PRINTS; PRO0010; EGFBLOOD.

PRINTS; PRO1217; PRICHEXTENSN.

SMART; SMO0179; EGF_CA; 3.

SMART; SM00001; EGF_1ke; 2.

PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_3.

PROSITE; PS001022; EGF_1; 5.

PROSITE; PS01187; EGF_CA; 3.
                                                                                                                                                                                                                                        FlyBase; FBgn0031414; CG15388.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00008; EGF; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D., Pallin, B.Y., Brandon R., Andrews-Pfannkoch C., Baddwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                           Calcium-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003583; AAF51268.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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  8
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F-like domain; Glycoprotein; Repeat.
87786 MW; A654CDBE4FDF42B0 CRC64;
                                                                                                                                                                                                                                                                 P_rich_extensn.
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Smith H.O.,
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                                       Query Match
Best Local
                                Matches
                               Local Similarity
nes 7; Conserv
        2 XIXNQXCXQXLDDCCSXXCNXXNXC :|: :|:::|:| |::| :: :|
4 EIKGSNCEENVDECMSNPCQNGGLC
                               Conservative
                                      53.3%;
                                       Score
Pred.
28
               26
                                Mismatches
                                      No .
                                     DB
1.3;
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                              5
                                              Length 838;
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Search completed: January 14, Job time: 30 secs

2003, 18:31:41

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Result
No.
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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140
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1: /SIDS2/gcgdata/c
2: /SIDS2/gcgdata/c
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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AAU10197
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ALIGNMENTS

Omega-conopeptide	ABB96887	23	26	45.0	63	5
of an	946	22	26	45.7	64	44
Analogue omega con	49	21	26	ÿ	64	43
Omega-conopeptide	437	21	26	Ġ	64	42
g omega	58	20	26		64	41
Conus genus analog	AAW72625	19	26	5	64	40
a conopepti	AAW12985	18	26	5	64	39
202, omega co	AAW19570	18	26	5	64	38
202. Synthet	AAR39628	14	26	45.7	64	37
	AAR37774	14	26	5	64	36
Omega-conopeptide	ABB96668	23	72	6	65	35
Omega-conopeptide	ABB96666	23	72	46.4	65	34
Omega-conopeptide	ABB96638	23	72	6.	65	33
	ABB96876	23	27	46.4	65	32
Omega-conopeptide	ABB96846	23	27	46.4	65	31
	ABB96774	23	27	46.4	65	30
1	ABB96786	23	26	6	65	29
	ABB96874	23	27	47.1	66	28
-conope	ABB96772	23	27	7.	66	27
Kappa-	AAU10195	22	27	۲	100	26
Kappa-	AAU10208	22	27	.4	118	25
. Kappa-	AAU10219	22	27	Ģ	120	24
Kappa-	AAU10215	22	27	5	120	23
. Kappa-	AAU10213	22	27	85.7	120	22
∟ Kappa-	AAU10211	22	27	5.	120	21
. Kappa-	AAU10209	22	27	5	120	20
Kappa	AAU10201	22	27	ŗ	120	19
l Kappa	AAU10216	22	27	7.	122	18
L Kappa-	AAU10210	22	27	87.1	122	17
Kappa-	AAU10205	22	27	7.	122	16
Kappa-	AAU10204	22	27	7	122	15
_	AAU10200	22	27	7.	122	14
_	AAU10214	22	27	87.9	123	13
	2	22	27	7.	123	12
Snail Kappa-conoto	AAU10217	22	27	88.6	124	11

## RESULT 1 AAU10196 ID AAU1 XX AU1 AX AU1 AX Snai XX Coni COX Syn: XX Coni OX Syn: YFT Mod FT Mod FT Mod FT MO FT WO2 XX W02 XX Y02 XX Z9: XX Z2: PR 20: XX Y02 XX Z2: PR 22: PR 22 Conus purpurascens. Synthetic. AAU10196 standard; peptide; cerebral ischaemia; ocular ischaemia; asthma; R18A. Snail Kappa-conotoxin PVIIA analogue R18A. AAU10196; 22-SEP-1999; 20-JUL-2000; 21-SEP-2000; 2000WO-US25827 WO200121648-A1 Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac i 29-MAR-2001. Modified-site 16-JAN-2002 (first entry) Modified-site 99US-155135P 2000US-0219438 /note= "Hyroxyproline" 27 /note= "The C-terminus is either a carboxyl group or an amide group" Location/Qualifiers 27 B

ischaemia;

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RESULT 2
AAU10197
ID AAU1
AC AAU1
XX Snai
XX Purp
KW Carc
XX Conc
OS Conc
OS Synt
XX WO21
FT Modi
FT Modi
FT Modi
FT XX
FF R 22-1
YR 22-1
YR 22-1
YR 22-1
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PA (CON
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual comprises.
                                              Cornell-Bell AH,
                                                                                                                                      22-SEP-1999;
20-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
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                                                                                          (COGN-) COGNETIX
                                                                                                                                                                                                       21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardioactive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVIIA analogue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kappa-conotoxin PVIIA peptide
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                           RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snail; kappa-conotoxin PVIIA analogue; circulatory;
e; antlasthmatic; KATP channel activation; cardiac ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                    99US-155135P
2000US-0219438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                       2000WO-US25827
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                              Pemberton KE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pemberton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
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                                                                                                                                                                                                                                                                                                                                    "The C-terminus
amide group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVIIA analogue
                                                                                                                                                                                                                                                                                                                                                                                                        "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia;
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Pred. No. 5
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                                              Temple DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Temple
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.4e-09;
                                                                                                                                                                                                                                                                                                                                                           either a carboxyl group
                                              Layer RT,
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                                              McCabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
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                                                                                                                                                                                                                                                                                         Synthetic.
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                                         WPI; 2001-648090/74
                                                                                                                   22-SEP-1999;
20-JUL-2000;
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                                                                                                                                                                                                                                                                                                                         cerebral
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                                                                                             (COGN-) COGNETIX
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                                                                                                                                                                                                                                                                                                                         ischaemia;
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                                                                        AΗ,
                                                                                                                  99US-155135P
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Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a

to an individual a

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RESULT 4
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                                                                                                      Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K25A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
                                               Claim 1;
                                                                                                                                                                                                                                                                          Cornell-Bell AH,
    The invention
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20-JUL-2000;
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                                                                                            kappa-conotoxin
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                                                                                       PVIIA peptide
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amide group"
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                                             English.
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treating
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Pred. No. 5.4e-09;
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP
                                                                                                           Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conoccain PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention.
                                                                                        Claim
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20-JUL-2000;
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antiasthmatic; KATP channel activation; cardiac ischaemia;
aemia; ocular ischaemia; asthma; O4A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
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81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                            "Hyroxyproline"
                                                                                       English.
                                                                                                                                                                                                              XΞ,
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RESULT 6
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Best Local S
Matches 21
                                          The present sequence represents a new kappa-conotoxin PVIIA which targets potassium channels and can be used to augment neurotransmitter release in pathological situations such as autoimmune diseases, e.g. Alzheimer's disease, Lambert-Eaton syndrome or myasthenia gravis. This peptide together with delta-conotoxin PVIIA act synergistically to rapidly immobilize fish which are injected with the two peptides. Injection of kappa-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This "fin-popping" occurs repeatedly resulting in a series of jerky movements, but injection of only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention.
                                                                                                                                                                                                                                                                                                                                                                                         can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conus
                      kappa-conotoxin PVIIA does not immobilize or kill the fish
                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                New
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augment neurotransmitter
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                                                                                                                                                                                                                                                                                                                29pp; English.
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77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potassium channel; neurotransmitter release;
lfish; delta-conotoxin PVIIA; disulphide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "disulphide bond"
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Pred. No. 5.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                       target potassium channels and
ter release in e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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Best Loc Matches Query Match

Local

Similarity 21; Conser

Conservative

89.3%; 77.8%;

Score 125; DB 22; Pred. No. 1.6e-08; 1; Mismatches 5;

Length

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Indels

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Best Local S
Matches 21
                              depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially caddical ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                    WPI;
Sequence
                                                                                                                                                                       membrane e.g. cardiac, cerebral and comprises activating a KATP channel
                                                                                                                                                                                                                                                                                                  22-SEP-1999; 99US-155135P
20-JUL-2000; 2000US-0219438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebral ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardioactive;
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                      PVIIA
                                                                                                                The invention relates to treating
                                                                                                                                       Claim
                                                                                                                                                           kappa-conotoxin PVIIA peptide
                                                                                                                                                                                              Treating disorders associated with radical
                                                                                                                                                                                                                                           Jones
                                                                                                                                                                                                                                                       Cornell-Bell AH,
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                      analogue
                                                                                                                                    1; Page 27; 46pp; English.
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27
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or an amide group"
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                        the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocular ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.78;
                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Hyroxyproline"
                                                                                                                                                                                                                                                       Æ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KATP channel activation; cardiac ischaemia; schaemia; asthma; R2K.
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Pred. No. 9.4e-09;
0; Mismatches 6
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                                                                                                                                                                                                                                                      Temple
                                                                                                                disorders associated with
                                                                                                                                                                    radical depolarization of excitable ocular ischaemia and asthma by administering to an individual a
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                                                                                                                                                                       and asthma
to an individual a
                                                                                                                 radical
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Best Local S
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                                                                                                          The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention.
                                                                                        Sequence
                                                                                                                                                                                                                          Claim 1; Page 28;
                                                                                                                                                                                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual kappa-conotoxin PVIIA peptide -
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20-JUL-2000;
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Modified-site
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CRIXNOKCYQHLDDCCSRKCNRFNKCV
         CRIXNQKCFQHLDDCCSXXCNXXNXCV 27
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                                                       Similarity
                                                                                        27
                                             Conservative
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27
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or an amide group"
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                                                                                                                                                                                                                         46pp; English.
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                                                     89.3%;
77.8%;
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                                                      Score 125;
Pred. No. 1
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                                                      DB 22;
.6e-08;
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                                         Gaps
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RESULT 10 AAU10207 ID AAU10 XX

AAU10207 standard;

peptide;

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CRIXNQKCFQHLDDCCARKCNRFNKCV 27

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RESULT 9
AAU10212
ID AAU1
XX AAU1
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DE Snai
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Qy
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Best Local
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                                                                                                                                                                                                                          depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin
                                                                                                                                                                                                            PVIIA analogue of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 28; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and coular ischaemia and asthma comprises activating a KATP channel by administering to an individual kappa-conotoxin PVIIA peptide -
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                                                                                                                                                              Sequence
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20-JUL-2000;
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21; Conser
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                                                        Conservative
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pemberton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an amide group"
                                                                                89.3%;
77.8%;
                                                                                                                                                                                                            invention.
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                                                                           Score 125; DB 22;
Pred. No. 1.6e-08;
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                                                                                                   Length
                                                   Indels
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                                                                                                      27;
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                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                 radical
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                                                Gaps
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RESULT 11
AAU10217
ID AAU10
XX
AC AAU10
XX
DT 16-JA
XX
DE Snail
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                                                                                                                                                           Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conus purpurascens Synthetic.
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                                                                                                                                                                                                                                                                                                                                       Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerebral ischaemia;
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                                                                                                                                                                                                                                                                                                           Claim 1; Page 28;
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20-JUL-2000; 2000US-0219438
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  Snail
                    16-JAN-2002
                                        AAU10217
                                                          AAU10217 standard;
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                          PVIIA analogue of the
                                                                                                                                                                                                                                                                                                                              kappa-conotoxin PVIIA peptide -
                                                                                                                                                                                                                                                                                                                                                                                                  Jones
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Kappa-conotoxin
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21; Conserv
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27
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                                                                                                                                                                                                                                                                                                          46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Pemberton
                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocular ischaemia; asthma; R2Q
                                                                                                                                                           88.6%;
77.8%;
 PVIIA analogue
                                                                                                                                                                                                            invention.
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                                                            27
                                                                                                                                                           Score 124; DB 22.
Pred. No. 2.1e-08
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                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Temple DL,
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   V27A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  either a carboxyl group
                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                           Layer
                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                            RT,
                                                                                                                                                                                                                                                                                                                                                                                                            McCabe
                                                                                                                                                 0;
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                                                                                                                   RESULT 12
AAU10198
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Best Local
           Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; I3A.
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones
                                                 Snail Kappa-conotoxin PVIIA analogue
                                                                                                            AAU10198
                                                                     16-JAN-2002
                                                                                         AAU10198
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The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conoctoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conoctoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerebral ischaemia; ocular ischaemia; asthma; V27A.
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20-JUL-2000;
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                                                                                                         CRIXNQKCFQHLDDCCSRKCNRFNKC
                                                                                                                                                                                                             Similarity
standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 28;
                                                                                                                                                                                                                                                                                                                      and asthma. The present sequence logue of the invention.
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                                                                                                                                                                                           Conservative
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or an amide group"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46pp; English.
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peptide;
                                                                                                                                                                                                             88.6%;
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                                                                                                                                                                                       Score 124; DE Pred. No. 2.1e 0; Mismatches
                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DL,
                                                                                                                                                                                         DB 22;
1.1e-08;
les 5;
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                                                                                                                                                                                                                                                                                                                                          is a kappa-conotoxin
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AAU10214
ID AAU1
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Best Local
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                             Purple cone snail; kappa-conotoxin PVIIA analogue; cir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 27; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-1999; 99US-155135P
20-JUL-2000; 2000US-0219438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000; 2000WO-US25827
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  Key
Modified-site
                                                                            Synthetic
                                                                                                    Conus purpurascens
                                                                                                                                                        cerebral ischaemia;
                                                                                                                                                                                                                                                       Snail Kappa-conotoxin PVIIA analogue L12A.
                                                                                                                                                                                                                                                                                                            16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                              AAU10214;
                                                                                                                                                                                                                                                                                                                                                                                                          AAU10214 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVIIA analogue of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kappa-conotoxin PVIIA peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COGN-) COGNETIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRIXNQKCFQHLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRAXNQKCFQHLDDCCSRKCNRFNKCV 27
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21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
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       Location/Qualifiers
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                                                                                                                                                        sthmatic; KATP channel activatic ocular ischaemia; asthma; L12A.
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77.8%;
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Pred. No. 2.8e-08;
0; Mismatches 6
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                                                                                                                                                                                                          circulatory;
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                                                                                                                                                                                cardiac
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                                                                                                                                                                                ischaemia;
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVITA (kappa-PVITA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac i cerebral ischaemia; ocular ischaemia; asthma; R2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
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                                                                                     Conus purpurascens Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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20-JUL-2000;
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                                Modified-site
                                                                                                                                                                  Snail Kappa-conotoxin
                                                                                                                                                                                             16-JAN-2002
                                                                                                                                                                                                                  AAU10200
                                                                                                                                                                                                                                        AAU10200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                 PVIIA analogue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to treating disorders associated with radical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kappa-conotoxin PVIIA peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COGN-) COGNETIX INC.
                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                             1 CRIXNOKCFQHLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                 CRIXNQKCFQHADDCCSRKCNRFNKCV
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 28;
                                                                                                                                                                                                                                                                                                                                                                                                                             and asthma.
                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                              Conservative
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                               /note=
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      /note= "The C-terminus is either a carboxyl group
or an amide group"
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                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                        peptide;
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77.88;
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                                                                                                                                                                     PVIIA analogue
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                                        "Hyroxyproline"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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Pred. No. 2
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.8e-08;
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                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                             kappa-conotoxin
                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                    cardiac ischaemia;
                                                                                                                                                                                                                                                                                                                                                                     27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    individual a
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AAU10204
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XX AAU10
XX AAU10
XX AAU10
XX I6-JA
DT 16-JA
DE Sna11
XX Purph
KW cardi
KW cereb
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (Kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention.
21-SEP-2000; 2000WO-US25827
                         29-MAR-2001.
                                                                                                                                                                      Conus purpurascens Synthetic.
                                                                                                                                                                                                        Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory; cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia; cerebral ischaemia; ocular ischaemia; asthma; K7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
                                                   WO200121648-A1
                                                                                                      Modified-site
                                                                                                                                                                                                                                                            Snail Kappa-conotoxin PVIIA analogue K7A.
                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                          16-JAN-2002
                                                                                                                                                                                                                                                                                                                   AAU10204;
                                                                                                                                                                                                                                                                                                                                            AAU10204 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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20-JUL-2000;
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amide group"
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Query Match
Best Local Similarity
                                   Matches
                                                                                                                                 The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin putita analogue of the inventor.
                                                                                                                                                                                                                                                                                                        Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide -
                                                                                              Sequence
                                                                                                                       PVIIA analogue of the invention.
                                                                                                                                                                                                                                                                               Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-648090/74.
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Search completed: January 14, 2003, 18:28:10 Job time: 36 secs

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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-08-613-400A-19
US-08-965-918-19
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US-07-789-913-8
US-08-675-774-8
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US-08-613-432-18
US-08-185-432-18
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                                                                            HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
         NAME/KEY: Modified-
LOCATION: 4
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                   MOLECULE TYPE:
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ZIP: 200
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CITY: W
STATE:
                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                              TOPOLOGY:
                                                                  ORGANISM:
                                                                                                                                                LENGTH:
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•	`	Sequence 21, Ap	•	Sequence 21, Ap	•	`	29,	`	-	Sequence 21, Ap	-	•	Sequence 29, Ap	-	Sequence 2, Appl	•	Sequence 20, App
App1	Appl	Appl	Tdc	Appl	ppl	Appl	Appl	1dc	Appl	Appl	Appl	Appl	Appl	Appl	110	19	ğ

## ALIGNMENTS

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TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08,
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shon, Ki-Joon
APPLICANT: Grilley, Michelle
APPLICANT: Olivera, Baldomero
TITLE OF INVENTION: Conotoxin
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08619936
                                                                                                                                                                                                                                                       27 amino acids
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                                                                                                           Conus purpurascens
                                                                   Modified-site
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/product= "4Hyp"
/note= "Amino acid 4 may be 4-trans-hydroxyproline."
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rk Avenue, Suite 1000
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; INDIVIDUAL ISOLATE: US-07-789-913-19
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                                                                                                                                                   TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bitner, R
APPLICANT: Yamashiro
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                            TYPE: AMINO ACID
TOPOLOGY: bo+b
TOLEFORM
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07 AUG-1990 PRIOR APPLICATION DATA:
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                              ORIGINAL SOURCE:
                                            ANTI-SENSE:
                                                        HYPOTHETICAL:
                                                                      MOLECULE TYPE:
                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           FILING DATE: 22-NOV-1989 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/789,913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
STATE: CA
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Local Similarity 81.5%;
Les 22; Conservative
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350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bitner, Robert S.
Yamashiro, Donald H.
YBNTION: Delayed Treatment Method of Reducing
VENTION: Ischemia-Related Neuronal Damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Bowersox, Stephen S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fox, James A.
Valentino, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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1..16
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15..26
                                                                                                                                                                                   (415) 324-0880
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                                                                                                                                              5) 324-0960
324-0960
NO: 19:
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              SNX-202
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Pred. No. 1.1e-09;
0; Mismatches 5
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US-08-049-794-19
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                                                                                                              ; INDIVIDUAL ISOLATE: US-08-049-794-19
                                                                   Query Match
Best Local :
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                                                      Matches
                                                                                                                                                                                                                                                                                                                                  APPLIANCE 1993U41.
FILING DATE: 1993U41.
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
APPLICATION NUMBER: 30-DEC-1991
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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AMDDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                          ORIGINAL SOURCE
                                                                                                                                                    MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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STATE: CA
                                                   Local Similarity es 9; Conserv
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 58
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FILING DATE: 19930415
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                                                                                                                                                                                                                                                                                                                          NAME: Stratford, Carol A.
                          1 CRIXNQKCFQHLDDCCSXXCNXXNXC 26
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1 CKLKGQSCSRLMYDCCSGSCGRSGKC
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5587454
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GOHIL, KISHOR C
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                                                      Conservative
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Pred. No.
                                                                  Score 64;
Pred. No.
                                                      Mismatches
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26
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0.059;
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RESULT 4 US-08-496-847-19

Sequence 19, Application US/08496847 Patent No. 5795864

MEDIUM TYPE:

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RESULT 5
US-08-742-774-19
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                                                                                                                                                                                                                                                       Sequence 19
Patent No.
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Best Local :
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                                                                                                                                                                                                                                          GENERAL
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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ADDRESSEE: Dehlinger & Associates
                                                                                                                            APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-0880
                                                                                                                    NUMBER OF SEQUENCES:
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COMPUTER READABLE FORM:
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OPERATING SYSTEM:
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                          COUNTRY:
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5824645
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9; Conservative
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                                                       Palo Alto
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N: 514
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, Stephen S.
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Pred. No. 0.059;
4; Mismatches
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Best Local Similarity
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                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
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                PRIOR APPLICATION DATA:
                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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CITY: Palo Alto
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                             APPLICATION NUMBER: FILING DATE: 03-JUI
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APPLICATION NUMBER:
                                CLASSIFICATION:
                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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MILJANICH, GEORGE P
AVENTION: METHODS OF PRODUCING ANALGESIA AND
AVENTION: ENHANCING OPIATE ANALGESIA
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                                           UMBER: US/08/675,354
03-JUL-1996
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US/08/049,794
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Pred. No. 0.
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0.059;
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FILING DATE: 1993-APPLICATION NUMBER:

1993-APR-15

US 07/814,759

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Best Local Similarity
""+"hes 9; Conserv:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino Type:
                                                                                              TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GOhil, National Peter 1.
APPLICANT: Additionssens, Peter 1.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MODI, JUDY M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: PI
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: //** `` 'TELEPHONE'
                MOLECULE TYPE:
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                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94306-1546
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5891849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amstutz, Gary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                            IBM Compatible
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                                                                                                                              650-324-0880
protein
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0.059;
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                                                                                              US-09-138-439-19
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                              Query Match
Best Local S
Matches 9
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Best Local Similarity 34.6%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                      TELEFAX: (415) 324-096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                           HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPLATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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CITY: Palo Alto
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                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1993-APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                           INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
1 CRIXNQKCFQHLDDCCSXXCNXXNXC 26
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                                Similarity
9; Conserv
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                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                         26 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SINGH, TEJINDER GOHIL, KISHOR C
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUSTICE,
                                                                                                                                                                        linear
                                                                                                                                           : protein
                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1991
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                                             45.7%;
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                                                                                                           SNX-202, FIGURE
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                                                                                                                                                                                                                                                                                                               34,444
                             ; Score 64; DB; Pred. No. 0.05
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Pred. No. 0.059;
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                                               0.059;
                                                          DB 2; Length 26;
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; INDIVIDUAL ISOLATE: SNX-202, FIGURE US-08-613-400A-19
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                                                                                                                                                                                                                                                                                                                               Patent No. 6087091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                          APPLICANT: JUSTICE, AMERICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: WILJANICH, GEORGE P
APPLICANT: MILJANICH, NALGESIA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: p:
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stratford, Carol REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKLKGQSCSRLMYDCCSGSCGRSGKC 26
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IMPROVED EPIDURAL
METHOD OF PRODUCING ANALGESIA
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                                      ENHANCING OPIATE ANALGESIA
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Pred. No. 0
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0.059;
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                                                                                                                                                                                                                                                                Sequence 19,
Patent No. 6
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
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REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                             TITLE OF INVENTION: METHODS OF PRODUCING ANALG: TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
                                                                                                                                                              APPLICANT: VALENTINO, KAREN L APPLICANT: MILJANICH, GEORGE P
                               STREET: 350 CTTY: Palo Alto
                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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 ZIP:
            COUNTRY:
                                                                               ADDRESSEE:
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94306
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                                                            350 Cambridge Avenue,
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               USA
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GOHIL, KISHOR C
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SYSTEM: PC-DOS/MS-DOS
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                                                            Law Offices of Peter Dehlinger 0 Cambridge Avenue, Suite 300
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                                                                                                                                                METHODS OF PRODUCING ANALGESIA AND
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Pred. No.
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US

US/09/392,979A

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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RESULT 12
US-07-789-913-8
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Best Local Similarity
----hes 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8,
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APPLICANT: Miljan
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                                                                                           APPLICATION NUMBER: US 0: FILING DATE: 02-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            STREET: 350
CITY: Palo Alto
CTATE: CA
                                                                                                                                                                                                            SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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LENGTH: 26 amino acids
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APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
REFERENCE/DOCKET NUMBER:
                 REGISTRATION NUMBER:
                                                                              APPLICATION NUMBER:
                                                                                                                                                                               APPLICATION NUMBER: UPPLING DATE: 19911112
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REFERENCE/DOCKET NUMBER: 5865-0009.30
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                              Stratford, Carol A.
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350 Cambridge Avenue, Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miljanich, George P. Bowersox, Stephen S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bitner, Robert
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                                                                JMBER: US 07/440,094
22-NOV-1989
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Ischemia-Related Neuronal Damage
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5865-0005.30
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                                                                                                                                                                                                                           Version #1.25
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; INDIVIDUAL ISOLATE: US-08-049-794-8
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Best Local Similarity 34...
Conservative
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Patent No.
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                                                                                                                  TELEFAX: (415) 324-096
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
                            MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 5865-0009.30 TELECOMMUNICATION INFORMATION:
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APPLICANT:
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APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
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APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
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                                                                             TOPOLOGY:
                                                                                         TYPE: AMINO ACID
                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                        TELEPHONE: (415) 324-0880
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AMINO ACID
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GOHIL, KISHOR C
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324-0960
8:
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        SVIB/SNX-183, FIGURE 1
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Pred. No.
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                                                                             RESULT 15
US-08-742-774-8
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US-08-496-847-8
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                                            Sequence 8, Application US/08742774 Patent No. 5824645
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
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Matches 9; Conservative
                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: pi
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-0880
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 APPLICANT:
                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 27-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stratford, Carol A REGISTRATION NUMBER: 34,444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CRIXNQKCFQHLDDCCSXXCNXXNXC 26
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JUSTICE, ALAN SINGH, TEJINDER
                                                                                                                                                                                                                                                                                                                                                                                                                                    650-324-0960
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34.6%;
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Pred. No. 0.18;
3; Mismatches
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Pred. No.
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                                                                                                         Query Match
Best Local Similarity
"~+~hes 9; Conserv
                                                                                                                                                                                     ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1 US-08-742-774-8
Search completed: January 14, 2003, 18:29:47 Job time: 15 secs
                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 324-09 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                 HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/00 FILLING DATE: 1993-APR-15 APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stratford, Car
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 94306
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                                                                                                                                                                                                                                                                                TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 5865-0009.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 03-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                        1 CRIXNQKCFQHLDDCCSXXCNXXNXC 26
                                                           CKLKGQSCRKTSYDCCSGSCGRSGKC 26
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VALENTINO, KAREN L
MILJANICH, GEORGE P
MILJANICH, GEORGE P
AVENTION: METHODS OF PRODUCING ANALGESIA AND
VENTION: ENHANCING OPIATE ANALGESIA
EQUENCES: 34
                                                                                                                                                                                                                                                                                           26 amino acids
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                                                                                                                         Conservative
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                                                                                                                                                                                                                                   NO NO
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30-DEC-1991
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324-0960
300: 8:
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                                                                                                                                      42.98;
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                                                                                                                      Score 60; DB Pred. No. 0.18 3; Mismatches
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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Maximum DB
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                seq length: 0 seq length: 2000000000
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Match
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
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          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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  US-09-894-882-120
US-09-894-882-211
US-09-894-882-210
US-09-894-882-210
US-09-894-882-201
US-09-894-882-201
US-09-894-882-201
US-09-894-882-306
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US-09-894-882-305
US-09-894-882-305
US-09-894-882-35
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Sequence 120, App
Sequence 168, App
Sequence 210, App
Sequence 210, App
Sequence 201, App
Sequence 201, App
Sequence 211, App
Sequence 211, App
Sequence 201, App
Sequence 201, App
Sequence 201, App
Sequence 200, App
Sequence 200, App
Sequence 305, App
Sequence 167, App
Sequence 175, App
Sequence 159, App
Sequence 159, App
Sequence 159, App
Sequence 159, App
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9	9	9	49.5	9	49.5	49.5	49.5	50	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	51.5	51.5	51.5	51.5	51.5
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36	36	36	36	36	36	35	29	176	76	75	75	71	70	42	42	42	42	36	36	3 <u>5</u>	70	37	36	36	36
10	10	10	10	10	10	10	ဖ	9	9	10	10	10	10	10	10	5	10	10	10	10	10	10	10	10	10
-894-882-37	-885	-882	US-09-894-882-365	US-09-894-882-207	US-09-894-882-165	88	37A-	US-10-024-599-4	US-09-749-637A-207	US-09-894-882-311	US-09-894-882-308	4	-89	NO.	<b>28</b> +	4-882	US-09-894-882-309	-894-882	-894-887	-882	-894-882	-882-22	-882-40	US-09-894-882-177	US-09-894-882-174
372,	371,	368,	Sequence 365, App	207,		,	208	Sequence 4, Appli		311	308	74,			449		Sequence 309, App	406		433				Sequence 177, App	

## ALIGNMENTS

us-09-894-882-120

Sequence 120, Application US/09894882 Patent No. US20020102607A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.

Cognetix, Inc. Walker, Craig S. Shetty, Reshma

; ORGANISM: Conus magus
; PERTURE:
; PERTURE:
; PARME/RERY: PEPTIDE
; LOCATION: (1)...(35)
; OTHER INFORMATION: Xaa at residue 33 is Pro or hydroxy-Pro; Xaa at residue 25
; OTHER INFORMATION: or gamma-carboxy-Glu; Xaa at residue 18 is Trp or bromo-Tr
US-09-894-882-120 CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/9
PRIOR FILING DATE: 2000-10-20
PRIOR PPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR PILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR PILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29 APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jinenez, Elsie C.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Watkins, Maren
APPLICANT: Watkins, Maren
APPLICANT: Jones, Robert M.
APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238 NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 120
LENGTH: 35
TYPE: non LENGTH: 35

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RESULT 2
US-09-894-882-413
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR PRIOR PLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR APPLICATION NUMBER: US 60/264,256
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PRIOR APPLICATION NUMBER: US 60/264,256
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Best Local Similarity
Matches 10; Conserv
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SEQ ID NO 413
LENGTH: 35
TYPE: PRT
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                                                                                                                                                                                                                                                                               Patent No.
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    CURRENT APPLICATION NUMBER: US/09/894,882
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                                           TITLE OF INVENTION:
                                                                                                     APPLICANT:
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Local Similarity 37.0%;
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                                                                                                                                                                                                                                                                           68, Application US/09894882
US20020102607x1
                                                                                            Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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Shetty, Reshma
                                                     Shen, Greg S.
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McIntosh, J. Michael
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                                                                             Robert M.
                                        I-Superfamily Conotoxins
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ORGANISM: Conus betulinus

FEATURE:

NAME/KRY: PEPTIDE

LOCATION: (1). (36)

OTHER INFORMATION: Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at resi

OTHER INFORMATION: 23 and 36 is Tyr, 1251-Tyr, mono-iodo-Tyr, di-iodo-Tyr,

OTHER INFORMATION: 0-Tyr or O-phospho-Ty

US-09-894-882-168
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PRIOR FILLING DATE: 2000-06-30
PRIOR PELICATION NUMBER: US 60/243,410
PRIOR FILLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/264,256
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2011-01-29
NUMBER OF SEQ ID NOS: 506
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NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 210
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Best Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shen, Greg S. TITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2314-238
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                                                                         LENGTH: 36
TYPE: PRT
ORGANISM: Conus lynceus
LOCATION: (1)..(36)
OTHER INFORMATION: Xaa at residues 2 and 4 is Trp or bromo-Trp; Xaa at residue
                                                              FEATURE:
                                        NAME/KEY: PEPTIDE
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McIntosh, J. Michael
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Shetty, Reshma
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Watkins, Maren
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Pred. No. 0.14;
3; Mismatches 11;
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US-09-894-882-404
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US-09-894-882-404
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/246,581
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Patent No. US20020102607A1
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Best Local Similarity
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APPLICANT:
APPLICANT:
                                                             APPLICANT: University of Utah Research Foundation APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Walker, Keshma
APPLICANT: Jimenez, Elsie C.
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APPLICANT:
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CURRENT FILING DATE: 2001-06-29
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PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
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                                  APPLICANT:
                                                  APPLICANT:
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Walker, Craig S.
Shetty, Reshma
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Shen, Greg S.
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Olivera, Baldomero M.
Watkins, Maren
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            McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
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Pred. No. 0.
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; ORGANISM: Conus magus US-09-894-882-119
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                                                        SOFTWARE: PatentIn
SEQ ID NO 119
LENGTH: 71
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Best Local Similarity 40.7%;
Matches 11; Conservative
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NUMBER OF SEQ ID NOS: 506
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PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
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PRIOR FILING DATE: 2000-06-30
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CURRENT FILING DATE: 2001-06-29
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
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Shen, Greg S.
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Watkins, Maren
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Shetty, Reshma
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l Similarity 37.0

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Score 56.5; DB Pred. No. 0.26; 2; Mismatches

DB 10; 26; 14;

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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
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PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
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                    APPLICANT:
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LOCATION: (1)..(36)
OTHER INFORMATION: xaa at residue 20 is Glu or gamma-carboxy-Glu; xaa at residues OTHER INFORMATION: and 4 is Trp or bromo-Trp; Xaa at residue 25 is Tyr, 125I-Tyr, OTHER INFORMATION: no-iodo-Tyr, di-iodo-Tyr, o-sulpho-Tyr or O-phospho-Ty
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PRIOR FILING DATE: 2000-06-30
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CURRENT FILING DATE: 2001-06-29
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12; Conserva
 INVENTION:
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US20020102607A1
                                            Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
Watkins, Maren
                 Shen,
                             Jones,
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                 Greg S.
                               Robert M.
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I-Superfamily Conotoxins
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Pred. No. 0.
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; LOCATION: (1)..(42)
; OTHER INFORMATION: Xaa at residue 36 is Pro or hydroxy-Pro; Xaa at residue 12 is
; OTHER INFORMATION: or gamma-carboxy-Glu; Xaa at residues 3 and 8 is Trp or bromo-
; OTHER INFORMATION: p; Xaa at residue 34 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-
; OTHER INFORMATION: , O-sulpho-Tyr or O-phospho-Ty
US-09-894-882-306
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PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
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PRIOR FILING DATE: 2000-06-30
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CURRENT FILING DATE: 2001-06-29
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PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
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NUMBER OF SEQ ID NOS: 506
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                                                                                             NAME/KEY:
LOCATION:
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
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                                    APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
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NUMBER OF SEQ ID NOS: 506
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TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
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FILING DATE: 2000-11-08
APPLICATION NUMBER: US 60/247,714
FILING DATE: 2000-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/264,256
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                                                                                                                                                                             INFORMATION
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P: Jones, Robert M.
P: Shen, Greg S.
INVENTION: I-Superfamily Conotoxins
                                                             Jimenez, Elsie C.
McIntosh, J. Michael
Olivera, Baldomero M.
                                                                                                          Cognetix, Inc.
Walker, Craig S.
Shetty, Reshma
                                                   Watkins, Maren
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McIntosh, J. Michael
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Shetty, Reshma
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SOFTWARE: Patentin version 3.0
SEQ ID NO 200
LENGTH: 70
                                                    Query Match
Best Local
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
                                                                                                                                                                                         SOFTWARE: PatentIn
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PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/264,256
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                                                                                                                                      TYPE: PRT
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1 CRIXNQKCFQHLDDCCSXXCNXXNXCV 27
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Watkins, Maren
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Jimenez, Elsie C.
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                                   Conservative
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39 CSWSGQEC-KHVSDCCGSFCCVGKRCL

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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/246,581
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NUMBER: US 60/264,256
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 369
LENGTH: 36
TYPE: PRT
ORGANISM: Conus betulinus
US-09-894-882-369
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US-09-894-882-167
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FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/246,581

PRIOR APPLICATION NUMBER: US 60/246,581

PRIOR FILING DATE: 2000-11-08
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins
FILE REFERENCE: 2314-238
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Local Similarity 37.0%;
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Olivera, Baldomero M.
Watkins, Maren
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Shen, Greg S.
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McIntosh, J. Michael
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PatentIn version 3.0
SEQ ID NO 167
LENGTH: 73
                                                     Query Match
Best Local Similarity 37.0
Matches 10; Conservative
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39 CLSLGORCERH-SDCCGYLCCFYDKCV 64
                          1 CRIXNOKCFOHLDDCCSXXCNXXNXCV 27
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Search completed: January 14, 2003, 18:30:04 Job time: 11 secs

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pir3:*
pir4:*
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  2003, 18:27:06 ;
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                                                                                                          A49128
E86452
T22025
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S45306
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S18188
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(without alignments)
173.042 Million cell upd
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conotoxin-like pro
conotoxin-like pro
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notch protein -
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45	45	45	45.5	45.5	46	46	46	46	46.5	47	47	47	47	47	47
32.1	32.1	32.1	32.5	32.5	32.9	32.9	32.9	32.9	33.2	33.6	33.6	33.6	33.6	33.6	33.6
570	138	29	503	99	1687	722	644	25	53	1480	1469	1064	880	833	832
N	2	N	N	N	N	N	N	N	N	N	N	Ν	N	N	N
A48836	H64561	A58537	G85432	T26416	T30176	<b>I48324</b>	S64135	JH0701	C72850	A36665	B36665	A40136	S00670	S19087	A31246
fibropellin C prec	invalid gene - Hel	omega-conotoxin MV	transcription init	hypothetical prote	EGF repeat transme	DELTA-like 1 - mou	hypothetical prote	omega-conotoxin MV	conotoxin homolog	slit protein 1 pre	otein	=			neurogenic protein

## ALIGNMENTS

A; Molecule type: protein
A; Residues: 1-27 <TRE>.
C; Comment: This conotoxin blocks conductance of the Shaker potassium channel.
C; Keywords: hydroxyproline; neurotoxin; venom
C; Keywords: 4-hydroxyproline (Pro) #status experimental kappa-conotoxin PVIIA - cone shell (Conus purpurascens)
N;Alternate names: fin-popping peptide
C;Species: Conus purpurascens (purple cone)
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999 Ş R;Terlau, H.; Shon, K.J.; Grilley, M.; Stocker, M.; Stuehmer, W.; Olivera, B.M. Nature 381, 148-151, 1996
A;Title: Strategy for rapid immobilization of prey by a fish-hunting marine snail. 뮹 RESULT A58997 A; Reference number: A58997 A; Accession: A58997 A;Status: preliminary C; Accession: A58997 Query Match Best Local S Matches 21 1 CRIPNOKCFQHLDDCCSRKCNRFNKCV Local Similarity 77.8 nes 21; Conservative 1 CRIXNOKCFQHLDDCCSXXCNXXNXCV 90.78; Score 127; DB 2; Le Pred. No. 6.6e-10; Pred. ---hes 6; 0; 27 Length 27; Indels 0; Gaps 0

RESULT C44379

omega-conotoxin SVIB [validated] - N; Alternate names: SNX-183 cone shell (Conus striatus)

C;Species: Conus striatus (striated cone)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 15-Sep-2000
C;Accession: C44379 G.C.; Nadasdi, L.; Hammerland, L.G.; Yoshikami, D.; Gray,

R;Ramilo, C.A.; Zafaralla, G Biochemistry 31, 9919-9926, A;Title: Novel alpha- and om A;Reference number: A44379; omega-conotoxins 9; MUID:93003172; 1992 from Conus striatus venom PMTD:1390774

A; Accession: C44379

A; Molecule type: protein
A; Residues: 1-26 < RAM>
A; Cross references: CAS:143306-19-8

A; Experimental source: venom
A; Note: sequence extracted from NCBI backbone (NCBIP:116002); s.
R; Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik,

structure confirmed k, D.J.

уd

submitted to the Brookhaven Protein Data Bank, August 1996 A; Reference number: A67649; PDB:1MVJ A; Contents: annotation; conformation by (1)H-NMR, residues R; Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; C.

J. Mol. | A;Title: R; Nielsen, K.J.; Thomas, L.; Lewis, R.J.; J. Mol. Biol. 263, 297-310, 1996 residues 1-26 P.F.; Craik, D.J

A consensus structure for omega-conotoxins with different selectivities for

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-2703 <KID>
A; Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1;
A; Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A58619; MUID:97070382; PMID:8913308
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: This omega-conotoxin blocks presynaptic calcium channels.
C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel
F;1-16,8-20,15-26/Disulfide bonds: #status predicted
F;26/Modified site: amidated carboxyl end (Cys) #status experimental
                                                                                                                                                      C;Accession: A24420; A24768; S09358; R;Kidd, S.; Kelley, M.R.; Young, M.W. Mol. Cell. Biol. 6, 3094-3108, 1986; A;Reference number: A24420; MUID:8706; A;Accession: A24420
                                                                                                                                                                                                                                     notch protein - fruit fly (Drosophila melanogaster)
N;Alternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24420; A24768; S09358; A05267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A35844; MUID:90385285; PMID:2402639 A;Accession: A35844
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F;184-215/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
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                    A; Reference number: A24768; MUID:86079539; PMID:3935325 A; Accession: A24768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;456-487/Domain:
F;757-788/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: transmembrane
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A; Residues: 1-2524 <COF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Coffman, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A35844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Date: 12-Oct-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1025-1056/Domain: EGF homology <EGX3>
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Best Local
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                                                        n, K.A.; Johansen, K.M.;
567-581, 1985
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type:
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9; Conserv
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9; Conserv
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EGF homology <EGX3>
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Pred. No. 0.21;
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Pred. No.
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sion 12-Oct-1990 #text_change 02-Aug-2002
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<AN3>
<AN4>
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R; Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Cell 40, 55-62, 1985
A;Title: opa: a novel family of transcribed repeats shared A; Reference number: A05267; MUID:85099329; PMID:2981631
A; Accession: A05267
A:Map position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384, 1679/3; 1729/1; 1761/3
C:Superfamily: unassigned EGF-related proteins; C:Keywords: receptor; signal transduction F:514-545/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                      R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, submitted to the EMBL Data Library, October 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 17, 6463-6471, 1989
A; Title: Hypervariability of simple sequences as a general source A; Reference number: S09358; MUID:89385974; PMID:2780284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-9 A; Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1964 < ROW>
                                                                                                                                                                                                                                                                                                          A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T09059
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F;1988-2004/Domain:
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F;1746-1762/Domain:
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A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
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                                                                                                                                               A; Gene: notch4
                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                                                                                                     A; Accession: T09059
                                                                                                                                                                                                                                                                                                                                   A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Mus musculus (house mouse);Date: 11-Jun-1999 #text_change 11-Jan-2000;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2538-2568/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .064-1095/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  824 QKCETNIDDCVTNPCGNGGTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 QKCFQHLDDCCSXXCNXXNXCV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2505-2551,'QQQQ',2552-2576,'E',2578-2604 <TAU>
                                                                                                                                                                                                                                                                                                          Sequence of mber: Z16543
                                                                                                 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF homology <EGX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transmembrane #status predicted
ankyrin repeat homology <AN1>
ankyrin repeat homology <AN2>
transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ankyrin repeat homology ankyrin repeat homology
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neurogenic repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF homology <EGF3>
                                                                                                                                                                                           EMBL: AF030001; NID: g2564945; PID: g2564947
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                                                                                                                                                                                                                                                                                                                              the mouse major histocompatibility locus class III region
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Pred.
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19;
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                                                EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2703;
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                                                                                                 577/1; 618/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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C; Species: Brachydan;
C; Date: 20-Feb-1995;
C; Accession: S42612
R; Bierkamp, C; Campo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-2437 <BIE>
A; Cross-references: EMBL:X69088; NID:9433866; PIDN:CAA48831.1; PID:9433867
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
F; 755-786/Domain: EGF homology <EGF1>
F; 1023-1054/Domain: EGF homology <EGF2>
F; 1185-1216/Domain: EGF homology <EGF2>
F; 1185-1216/Domain: ankyrin repeat homology <AN1>
F; 1948-1980/Domain: ankyrin repeat homology <AN3>
F; 1948-2014/Domain: ankyrin repeat homology <AN3>
F; 2015-2047/Domain: ankyrin repeat homology <AN3>
F; 2015-2047/Domain: ankyrin repeat homology <AN3>
                                                                                                                                                                                                                                                                                                                                                                                                                            C:Accession: A40043
R:Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, Cell 66, 649-661, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: A zebrafish homologue of the Drosophila neurogenic A;Reference number: S42612; MUID:94128602; PMID:8297791 A;Accession: S42612
                                                                                                                                                                                                                                                                                                                                                                           A;Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosoma. A;Reference number: A40043; MUID:91347367; PMID:1831692
A;Accession: A40043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notch protein homolog TAN-1 precursor - human C;Species: Homo sapiens (man) C;Date: 21-Apr-1992 *sequence_revision 21-Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c;Species: Brachydanio rerio (zebra fish)
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-2555 <ELL>
A;Cross-references: GB:M73980
A;Cross-references: GB:M73980
C;Superfamily: notch protein; ankyrin x
F;261-292/Domain: EGF homology <EGX1>
F;261-292/Domain: EGF homology <EGX1>
F;494-525/Domain: EGF homology <EGX2>
F;987-1018/Domain: EGF homology <EGX2>
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                                                                                                                                        F;1927-1959/Domain:
                                                                                                                                                                                    F;1187-1218/Domain:
                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
Query Match
Best Local Similarity
                                                                                                                                                                                                      1149-1180/Domain:
                                                                                                                                                              1233-1264/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 CSENIDDCASAACSHGATC 349
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7; Conser
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                                                                                            : EGF homology <EGF>
: EGF homology <EGF3>
: EGF homology <EGF3>
: ankyrin repeat homology <
: ankyrin repeat homology <
: ankyrin repeat homology <
                                                           ankyrin
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                                                           repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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Pred. No.
Score
Pred.
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                                                                                                                                                                                                                                                                                   repeat homology;
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No.
  DB 2;
45;
                                                           <AN1>
<AN2>
<AN3>
<AN4>
<AN5>
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                      Length 2555;
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R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog
A;Reference number: A46019; MUID:93194170; PMID:8449489
A;Accession: A46019
A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2531 < DELLA
A;Molecule type: nucleic acid
A;Residues: 1-2531 < DELLA
A;Cross-references: GB:E11886; GB:S47228; NID:9288502; PIDN:CAA77941.1; PID:9288503
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J
submitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, sugg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1025-1056/Domain: EGF homology <EGF>
F;1033-1264/Domain: EGF homology <EGF2>
F;1233-1264/Domain: EGF homology <R072-
F;1917-1949/Domain: ankyrin repeat homology <AN2>
F;1950-1982/Domain: ankyrin repeat homology <AN2>
F;1984-2016/Domain: ankyrin repeat homology <AN3>
F;2017-2049/Domain: ankyrin repeat homology <AN4>
F;2017-2049/Domain: ankyrin repeat homology <AN5>
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A;Residues: 1-2531 <WEI>
A;Cross-references: EMBL:X57405; NID:g57634;
C;Superfamily: notch protein; ankyrin repeat
F;987-1018/Domain; EGF homology <EGF1>
F;987-1018/Domain; EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              notch protein homolog - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S18188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
C;Accession: A46019; S25144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Weinmaster, G.; Roberts, V.J.; Lemke, G. Development 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during A;Reference number: S18188; MUID:92111383; PMID:1764995
A;Accession: S18188
A;Note: proximal region of chromosome 2 C;Superfamily: unassigned ankyrin repeat F;106-138/Domain: EGF homology <EGF1>F;144-175/Domain: EGF homology <EG01>F;222-254/Domain: EGF homology <EGF2>
                                                                                                                                                                                                        A; Action type: mRNA
A; Rolecule type: mRNA
A; Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRAN
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Notch-1 protein - mouse
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                                                                                                                                                                                                                                                                                                                 A; Reference number: S25144
A; Accession: S25144
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                                                                                                                                          A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 QNCEENVDDCPGNNCKNGGACV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 8; Conserv
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3; Mi
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Pred. No.
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R; Farr-Jones, S.; Basus, V.J.
submitted to the Brookhaven Protein Data Bank, December 1994
A; Reference number: A66297; PDB:10MN
A; Contents: annotation; conformation by (1)H-NMR, residues 3-28
R; Farr-Jones, S.; Miljanich, G.P.; Nadasdi, L.; Ramachandran, J.; Basus, V.J.
J. Mol. Blol. 248, 106-124, 1995
A; Title: Solution structure of omega-conotoxin MYTIC, a high affinity of P-type calcium A; Reference number: A58582; MUID:95248539; PMID:7731037
A; Contents: annotation; conformation by (1)H-NMR
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:S40826; NID:g252126; PIDN:AAB22674.1; PID:g252127 R;Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, SBiochem. Biophys. Res. Commun. 207, 695-700, 1995 A;Title: Solution structure of omega-conotoxin MVIIC determined by NMR. A;Reference number: PC2380; MOID:93169113; PMID:7864862 A;Accession: PC2380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: JH0699; PC2380
R;Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramacha Neuron 9, 69-77, 1992
A;Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A;Reference number: JH0699; MUID:92337922; PMID:1352986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1025-1056/Domain:
F;1063-1094/Domain:
F;1149-1180/Domain:
                                                                          F; 3-28/Product:
                                                                                                C; Keywords:
                                                                                                                 C; Superfamily: omega-conotoxin
                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 3-28 < NEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-29 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      omega-conotoxin MVIIC precursor [validated] - cone shell (Conus magus) (fragment) (;Species: Conus magus (magus cone) C;Decies: Conus magus (magus cone) C;Date: 17-Apr-1933 #sequence_revision 11-Apr-1997 #text_change 15-Sep-2000 C;Accession: JH0699; PC2380
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F; 1233-1264/Domain:
F; 1352-1383/Domain:
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;339-370/Domain:
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Best Local
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Query Match
                                                       3-18,10-22,17-28/Disulfide
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                                                                                              acetylcholine release inhibition;
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8; Conser
                                                     omega-conotoxin MVIIC *status experimental -28/Disulfide bonds: *status experimental
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EGF homology <EG11>
EGF homology <EG12>
EGF homology <EG13>
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EGF homology <EG16>
EGF homology <EG17>
EGF homology <EG18>
EGF homology <EG18>
EGF homology <EG19>
EGF homology <EG19>
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homology <EG06>
homology <EG07>
homology <EG08>
homology <EG09>
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Pred. No.
Score 50;
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                                  (Cys) (amide
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<AN2>
<AN3>
<AN4>
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DB 2;
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                                                                                              amidated carboxyl
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Length 29,
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                     CSENIDDCAYASCTPGSTCI 37
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A;Cross-references: EMBL:x68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
A;Experimental source: embryo
A;Experimental source: embryo
A;Experimental source: embryo
A;Experimental source: embryo
A;Experimental source: embryo
A;Experimental source: embryo
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision be C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology CEGX1>
F;143-174/Domain: EGF homology CEGF1>
F;560-591/Domain: EGF homology CEGF2>
F;5760-791/Domain: EGF homology CEGF3>
F;7836-867/Domain: EGF homology CEGF3>
F;836-867/Domain: EGF homology CEGX3>
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submitted to the EMBL Data Library, November 1996
A;Reference number: Z19541
A;Accession: T22274
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                     R:Lardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A;Title: Motch A and Motch B--two mouse Notch homologues
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: A49175
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1203 <LAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: Z81540; PIDN: CAB04398.1; GSPDB: GN00023; CESP: F46B3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-354 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 20-Sep-1999
C;Accession: A49175; PH1570; S32113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F46B3.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Motch B protein - mouse (fragment) N; Alternate names: Notch homolog
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Best Local S
Matches 9
                                              Query Match
Best Local S
Matches 6
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8 CFQHLDDCCSXXCNXXNXCV
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32.1%;
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Pred. No.
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49;
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F;264-295/Domain: EGF homology <EGX1>F;799-830/Domain: EGF homology <EGF1>F;877-908/Domain: EGF homology <EGX2>
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Development 116, 93-041, 1992
A; Title: Notch2: a second mammalian Notch gene.
A; Reference number: A49128; MUID:93202015; PMID:1295745
                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Lin, Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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F;1191-1222/Domain:
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                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005172; NID:g6714280; PIDN:AAF25976.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-358 <STO>
                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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Residues: 1-2471 <WEI>
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172 CRVFRKKNYQKIDDC
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ankyrin repeat homology <AN3>
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46.7%;
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hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 18-Feb-2000
C;Accession: T22025
Search completed: January 14, 2003, 18:29:27 Job time: 17 secs
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submitted to the EMBL Data Library, February 1996
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A;Accession: T22025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                A;Gene: CESP:F40E10.4
                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
A;Experimental source: clone F40E10
                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-601 <WIL>
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                                                                                                                                                                                                                                       <u>M</u>00
                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA.", Biophys. J. 82:3003-3011(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular simulation of the interacthe Shaker potassium channel pore.",
Eur. Biophys. J. 30:528-536(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dependent."
                                                                                                                                                                                                                                                                                                                3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Naranjo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moran O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11820396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10398696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOCKADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12023223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                   CAUTION:
50, Leu-5
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Expressed by the venom duct.

MASS SPECTROMETRY: NN-3268.4; METHOD-FAB.

SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS

SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      potassium channels. The rat brain voltage-gated potassium channel protein Kv1. I is resistant to this toxin, but the voltage-gated potassium channel protein Shaker (Drosophila) is sensitive. The interaction site between the Shaker channel and this toxin is within the S5-S6 loop of the Shaker channel. In fish, this toxin induces hyperactivity, followed by continuous contraction and extension of major fins, without immobilization or death. Injection of this peptide together with the delta-conotoxin PVIA causes the sudden tetanus of prey (STOP) syndrome, which is a single, lethal "fin-pop" in envenomated fish. In mice, induces
                                                                                                                                                                                                                                                                                                                                                           with caution.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
                                                                                                                                                                                                                                                                                                                                                                     results of mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperactivity.
                                                                                                                                                                                                                                                                                                                                      1KCP; 14-0CT-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H., Boccaccio A.,
lock of Shaker K+,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiol. 114:125-140(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QF,
                                                                                                                                                                                                                                                                                                                             Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHAKER CHANNEL BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHAKER CHANNEL
                      Because analogs resulting of mutagenesis of Hyp-49, A
57 and Asp-59 gave very low yields upon folding, the
of mutagenesis on these residues should be interpreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHAKER-PVIIA INTERACTION
                                                                                                                                                                                                                                                                                                                Signal
                                                                                                                                                                                                                                                                                                                             Potassium
                      ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channels
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                                                                                                                                 P->A: 100% REDUCTION OF TOXICITY.
N->A: 100% REDUCTION OF TOXICITY
O->A: 1500% REDUCTION OF TOXICITY
K->A, M: 100% REDUCTION OF TOXICITY
F->A, M: 100% REDUCTION OF TOXICITY
F->Y: 11-FOLD DECREASE OF TOXICITY.
                                                                                                                                                                                                                                                                                                                        channel inhibitor; Hydroxylation;
                                                                                                                                                                                                        HYDROXYLATION.

R->A, K,Q: 100% REDUCTION OF TOXICITY

I->A: 3-FOLD DECREASE OF TOXICITY.
                                                                                                                                                                                                                                                                                 KAPPA-CONOTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interaction of kappa-conotoxin-PVIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVIIA
                                                 A: 3-FOLD DECREASE OF TOXICITY.
A: 3-FOLD DECREASE OF TOXICITY.
A: 1.00% REDUCTION OF TOXICITY.
A: 1.5-FOLD DECREASE OF TOXICITY.
A: 1.05-FOLD DECREASE OF TOXICITY.
A: 3.5-FOLD DECREASE OF TOXICITY.
A: 3.5-FOLD DECREASE OF TOXICITY.
A: 1.2-FOLD DECREASE OF TOXICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by kappa-conotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B.M., Conti F.;
                   17-FOLD DECREASE
19-FOLD DECREASE
         117-FOLD DECREASE
                                           5-FOLD DECREASE
                                          OF TOXICITY
                     ဝှင်
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                                       Amidation;
SIGNAL
PROPEP
                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97070382; PubMed-8913308; Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J. "A consensus structure for omega-conotoxins with different selectivities for voltage-sensitive calcium channel subtypes: comparison of MVIIA, SVIB and SNX-202."; J. Mol. Biol. 263:297-310(1996).
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"Novel alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom duct;
MEDLINE=20037955;
Lu B.-S., Yu F., Z
                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- FUNCTION: Omega-conotoxins act at presynaptic membranes, and block voltage-sensitive calcium channels (VSCC). Thi blocks N., P., and Q-type calcium channels.
-i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gasi
Neogastropoda; Conoidea; Conidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P28881: 09UB25;
01-DEC-1992 (Rel. 24, Created)
16-OCT-2001 (Rel. 40, Last sequence updat
15-JUN-2002 (Rel. 41, Last annotation upd
Omega-conotoxin SVIB precursor (SNX-183).
                                                                                                Pfam; PF02950; Conotoxin; 1.
Presynaptic neurotoxin; Neurotoxin; Toxin;
                                                                                                                                                                                                                                                        entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry
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Lu B.-S., Yu F., Zhao D., Huang P.-T.,
"Conopeptides from Conus striatus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY
                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                       LWVJ;
                                                                                                                                                                                              C44379; C44379
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                                                                                                                                                IPR004214; Conotoxin.
                                                                              Signal;
                                                                                                                                                                       12-AUG-97
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Pred. No. 3e-11;
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Miljanich G., Olivera B.M
                                                                                                     Calcium
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PEPTIDE DISULFID

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OMEGA-CONOTOXIN SVIB

3D-structure

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MEDLINE=90385285; PubMed=2402639;
Coffman C., Harris W., Kintner C.
"Xotch, the Xenopus homolog of Dr
Science 249:1438-1441(1990).
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M33874; AABO2039.1;
PIR; A35844; A35844.
HSSP; P00740; 1EDM.
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Submitted (JUN-1996) to
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                            ppf00008; EGF; 36.
; ppf00023; ank; 6.
;; ppf00063; notch; 3.
;; ppf00066; notch; 3.
TTS; pr00010; EGFBLOOD.
TTS; pr001452; NOTCH.
TT; SM00248; ANK; 5.
TT; SM00179; EGF_L1ke; 11
TT; SM00004; NL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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9; Conser
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Mesobatrachia; Pipoidea;
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01-NOV-1986 (Rel. 03, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus Notch protein precursor.
N OR Ec:140G11.1 OR Ec:163A10.2 OR CG3936.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilia.
NCBI_TaxID-7227;
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J. Biol. Chem. 275:35335-35344(2000)
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STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE-86079539; PubMed-3935325;
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Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L.,
Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.
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Conus catus (Cat cone).
Conus catus (Cat cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID-101291;
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15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last annomega-conotoxin CVIC.
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SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: EX
SIMILARITY: BELONGS TO
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RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Heasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,

RA Durbin K.J., Evanley S., Dahlke C., Davenport I.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrar S., Fleischmann W.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glann P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M., McLin D., Liai Z.,

RA Merkulov G., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Ran B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Wang Z.-Y., Wassarman D.A., Wainstock G.M., Weissenbach J.,

RA Wang S.-Y., Wassarman D.A., Wainstock G.M., Weissenbach J.,

RA Wang S.-Y., Wassarman D.A., Wainstock G.M., Weissenbach J.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA The Genome sequence of Drosophila melanogaster.";

RL Schence 287:2185-2195-2000).
                                                                                                                                                       MEDLINE-20196011; PubMed-10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Demailles J., Cadieu E
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E
Dreano S., Gloux S., Lelaure V., Mottler S., Gallbert F., Borkova
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papaglannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkloti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
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                                        melanogaster.
Science 287:2
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                                                                                                      Glover D.M.;
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Cell 43:567-581(1985).
    SEQUENCE OF
                                                                                                                       McMillan P.J.,
                                                                                                                                            Callister D.M.,
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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nce 287:2185-2195(2000).
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MEDLINE=87257846; Restriction of Pemelanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85099329; PubMed=2981631; Wharton K.A., Yedvobnick B., Finn
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(Suppressor of hairless) and activates genes of the enhancer of split locus. Essential for proper differentiation of ectoderm. SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: BELONGS TO THE NOTCH FAMILY. SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
                                                                                                                                                                                     FUNCTION: Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD)
                                                                                                                                                                                                                               C. Biol. 1:120-122(1991).
FUNCTION: Functions as a receptor
                                                                                                                                                               it forms a transcriptional activator complex with Su(H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF 1-8 FROM
                                                                                                                                                                                                                                                                                                                                                                       Biol.
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dd S., Berg R.L., You
P-element insertions
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use by non-profit modified and this st entities requires a This or send an email to license@isb-sib.ch). European Bioinformatics Institute. SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM statement is not removed. Usage by and fo a license agreement (See http://www.isb-sib. institutions as long as There are no rest restrictions EMBL outstation a collaboration for in 9

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EMBL; M16152; AAB59220.1; J EMBL; M16153; AAB59220.1; J EMBL; M16149; AAB59220.1; J EMBL; M16150; AAB59220.1; J EMBL; M16151; AAB59220.1; J EMBL; M35508; AAA28725.1; J EMBL; M35689; AAA28725.1; J EMBL; K35507; AAA28725.1; J EMBL; K35507; AAA28725.1; J EMBL; K35507; AAA2873610.1; EMBL; AL035436; CAB37610.1; EMBL; AL035436; CAB37610.1; InterPro; IPR0002110; ANK. InterPro; IPR000152; Asx.b. InterPro; IPR000561; EGF-1: InterPro; IPR000742; EGF-2: InterPro; IPR001881; EGF-C: InterPro; IPR001438; EGF-II InterPro; IPR0001438; EGF-II InterPro; IPR000800; Notch PRINTS; PRINTS; SMART; S EMBL; HSSP; P00740; FlyBase; FBgn AE003426; AAF45848.2; -.
AL035436; CAB37610.1; -.
AL035395; CAB37610.1; JOINED
M12175; AAA74496.1; -.
M16025; AAA28726.1; -. PF00066; SM00248; A SM00248; A SM00181; E SM00179; E SM00004; N PF00023; ank; 6 PF00066; notch; PF00008; EGF; 36. PR00010; FBgn0004647; A05267. A24768. A24420. 1EDM ANK; 7. EGF; 36. EGF\_CA; 35. NL; 2. EGFLAMININ NOTCH. EGFBLOOD σ Laminin\_EGF Asx\_hydroxyl. Notch ω JOINED.
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                                        Lewis R.J., Nielsen K.J., Craik D.J., Loug
Sharpe I.A., Luchian T., Adams D.J., Bond
Matheson J.-L., Drinkwater R., Andrews P.R
"Novel omega-conotoxins from Conus catus d
calcium Channel subtypes.";
J. Biol. Chem. 275:35335-35344(2000).
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Neogastropoda; Conoidea; Conic
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DOMAIN
                                                                                                                      PubMed=10938268;
                                                                                                                                  TISSUE-Venom
                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                         Omega-conotoxin CVID p
Conus catus (Cat cone)
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                                                                                                                                                                                                                                                                                                                                                                                            6
  and block vol
similarity).
                3101. Chem. 275:35335-35344(2000).
FUNCTION: Omega-conotoxins act at pr
and block voltage-sensitive calcium
                                                                                                                                                                                                                                                                                                     CONCT
                                                                                                                                                                                                                                                                                                                                                                 QKCETNIDDCVTNPCGNGGTCI
                                                                                                                                                                                                                                                                                                                                                                                          QKCFQHLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 36.4
8; Conservative
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PS01186;
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PS50297;
PS00010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01187; EGF_CA; 21.
Transcription regulation; Activator;
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                                                                                                                                duct,
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in; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                     STANDARD;
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ANK_REP_REGION;
ASK_HYDROXYL; 22;
EGF 1; 34.
; EGF_2; 28.
; EGF_CA; 21.
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                                                                                                                                 and Venom;
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                                                                                                                                                                                                                                     precursor.
  toxin
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Last annotation update)
                                                                                                                                                                                                 Conidae;
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dae; Conus.
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                            presynaptic membranes,
                                                                                                        Loughnan
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                                                                nd T., Thomas L
P.R., Alewood P
s discriminate
                channels
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    calcium
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Matches 8
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  mouse mammary
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TISSUB-Lung, and Testis;
TISSUB-Lung, and Testis;
MEDLINE-96281668; PubMed-8681805;
Merazzi G., Wu G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
16-JUN-2002 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 4 precursor
[Contains: Transforming protein Int-3].
                          SEQUENCE OF 1436-1600 FROM N.A. MEDLINE-99252212; PubMed-102339 Lee J.-S., Haruna T., Ishimoto
                                                                                                                                                                                 Uyttendaele H., Marazzi G., Wu G., Yan Q. "Notch4/int-3, a mammary proto-oncogene, cell-specific mammalian Notch gene.";
Development 122:2251-2259(1996).
                                                                                                                                                                                                                                                                                             Gallahan D., Callahan R.; "The mouse mammary tumor assuthe NOTCH gene family (NOTCH Concogene 14:1883-1890(1997).
                                                                                                              Rowen L., Mahairas G.,
Loretz C., Schmidt S.,
"Sequence of the mouse
                                                                                                                                                                                                                                                                                                                                                                                             Robbins J., Blondel B.J., Gallahan I
MOUSe mammary tumor gene int-3: a n
transforms mammary epithelial cells.
J. Virol. 66:2594-2599(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92194507; PubMed=1312643; Robbins J., Blondel B.J., Gallaha "Mouse mammary tumor gene int-3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-92194507;
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Eukaryota; Metazoa; C
                                                                                                                                                        SEQUENCE FROM N.A.
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8; Conser
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                                                                                  (OCT-1997)
             252212; PubMed=10233982;
Haruna T., Ishimoto A., Honjo
ernal type A particle-mediated
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                                                                                                                                                                                                                                                                                                                            tumor associated
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Rodentia;
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                                                                                                                                                                                                                                                                                                             (NOTCH4).";
                                                                                                            Qin S., Ahearn M.E., Dankers
Tipton S., Traicoff R., Zack
major histocompatibility locu
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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T., Yanagawa S.-I.;
activation of the Notch4/
n of truncated Notch4/int3
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, Zackrone K., Ho
Ly locus class II
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Proc. Natl Bash Soft
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"Murine notch
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                                                                                                                                                                                                                      - PTM: Phosphorylated.
- DISEASE: Loss of the extra activation of the Notch plof glandular epithelial to carcinomas.
- SIMILARITY: BELONGS TO THIS SIMILARITY: CONTAINS 3 LII-SIMILARITY: CONTAINS 5 ANII-SIMILARITY: CONTAINS 5 ANII-SIMILARITY: CONTAINS 5 ANII-SIMILARITY: CONTAINS 5 ANII-
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SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in he kidney, and at lower levels in the ovary and skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNT-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notth extracellular truncation (NEXT). This fragment is then cleaved by presentin dependent gamma-secretase to release a notth-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Netl. Acad. Sci. U.S.A. 98:9026-9031(2001).
FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBB-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May regulate branching morphogenesis in the developing vascular system.
SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide honds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during embryonic development from 9.0 d.p.c.
                                                                                                                                                                                                                                                                                                                                                                                                                          from the membrane
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                                                                                                                                                                                                                                                                                                                                   extracellular domain causes
tch protein, which leads to l
ial tissues and development o
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29 EGF-LIKE DOI
3 LIN/NOTCH REI
5 ANK REPEATS.
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iated with expression
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echanisms of
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f signal transduction
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         PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00104; GGF_Like; 15.
SMART; SM00001; EGF_Like; 15.
SMART; SM00004; NL; 2.
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_II.
InterPro; IPR000800; Notch.
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PRINTS; PR01415;
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AB016771; BAA32281.1;
AB016772; BAA32283.1;
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PS00010;
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EGF_1; 28.
EGF_2; 21.
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InterPro;
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01-NOV-1995 (Rel. 32,
15-JUN-2002 (Rel. 41,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                   InterPro;
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                                                                                                                                                                                                                                                       and differentiating mesoderm. Also present brain and head regions.
SIMILARITY: BELONGS TO THE NOTCH FAMILY.
SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 6 ANK REPEATS.
 4; ZDB-GENE-990415-173; n

xrPro; IPR002110; ANK,

xrPro; IPR000152; Asx_hyd

xrPro; IPR000561; EGF-1ik,

xrPro; IPR000742; EGF_2,

xrPro; IPR001881; EGF_Ca,

xrPro; IPR001438; EGF_II.
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                                                                                                             X69088; CAA48831.1;
P00740; 1EDM.
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os-Ortega J.A.;
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EGF_2.
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     Pfam; PF00023; ank; 6.

Pfam; PF00066; notch; 3.

PR PRINTS; PR00010; EGFBLOOD.

R PRINTS; PR01452; NOTCH.

SMART; SM00179; EGF_CA; 19.

SMART; SM00001; EGF_Like; 16.

SMART; SM00001; EGF_Like; 16.

SMART; SM00001; EGF_Like; 16.
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E; PS50297; ANK REP_REGION; 1
E; PS001010; ASK_HYDROXYL; 23.
E; PS00022; EGF_1; 34.
E; PS01186; EGF_2; 28.
E; PS01187; EGF_CA; 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription
                                          1487
1521
1867
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1982
2015
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                                          EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5. CALCIUM-BINDING (POTEN EGF-LIKE 6.
EGF-LIKE 7. CALCIUM-BINDING (POTEN EGF-LIKE 1).
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Best Local Similarity
Matches 7; Conserv
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Smith S.D., Sklar J.;
"TAN-1, the human homolog of
Chromosomal translocations i
Cell 66:649-661(1991).
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NTC1_HUMAN
P46531;
01-NOV-1995
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Submitted
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MEDLINE-99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsladis E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gray G.E., Mann R.S., Mitsiadis E., Henrique D. Banks A., Leiman J., Ward D., Ish-Horowitz D., "Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(1999).
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Mammalia; Eutheria;
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15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Neurogenic locus notch homolog protein
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                                                                                                                                                                                                                                                                       domain (NICD) it forms a transcriptional activator complex with Affects the implementation of differentiation, proliferation and approved to programs. May be important for normal lymphocyte function. In altered form, may contribute to transformation or progression in some T-cell neoplasms. Involved in the maturation of both CD4+ and CD8+ cells in the thymus (By similarity). SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity). Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus (By proteolytical processing NICD is translocated to the nucleus (By contributed to the nucleu
                 brain stem and lung. Also present in most adult tissues where it is found mainly in lymphoid tissues.

PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TMF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Deltal to regulate cell-fate determination Upon ligand activation through the released notch intracellular
                                                                                                                                                                                                                                  similarity).
TISSUE SPECIFICITY:
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Pfam; PF0000B; EGF; 36

Pfam; PF0000B; ank; 6.

Pfam; PF0000B; notch; 3.

Pfam; PF0000B; notch; 3.

SMART; SM00019; EGF_1ke; 13.

SMART; SM00001; EGF_1ke; 13.

SMART; SM00001; ML; 2.

PROSITE; PS5000B; ANK_REPEAT; 4.

PROSITE; PS500297; ANK_REP_REGIO PROSITE; PS50010; ASX_HYDROXYLL

PROSITE; PS00012; EGF_1; 34.

PROSITE; PS01187; EGF_2; 26.

PROSITE; PS01187; EGF_2; 18.

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PTM: Phosphorylated (By similarity).

DISEASE: Notch1 truncation is associated with neoplasia, a T-cel acute lymphoblastic leukemia.

SIMILARITY: BELONGS TO THE NOTCH FAMILY.

SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.

SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ifled and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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M73980; AAA60614.1; -.
P00740; 1EDM.
; HGNC:7881; NOTCH1.
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); IPR002110; ANK.

o; IPR000152; Asx_hydroxyl.

o; IPR000561; EGF-11ke.

ro; IPR000742; EGF_2.

'ro; IPR001881; EGF_Ca.

'ro; IPR001438; EGF_II.

-ronn0800; Notch.
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   Glycoprotein;
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; ANK_REP_RECION;
; ASX_HYDROXYL; 20
; EGF_1; 34
; EGF_2; 26
; EGF_CA; 18
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2556
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Pfam; PF00008; EGF; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boulter J., Greenfield A., Weinmaster G.; "Rattus norvegicus mRNA for Delta 3: a putative ligand for Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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PS01186; EGF_2;
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16-OCT-2001 (Rel. 40 0-16-OCT)
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16-OCT-2001 (Rel. 40, Last sequence up
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Delta-like protein 3 precursor (Drosop
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TISSUE-Neural
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Bulotsky M.S., Spencer
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Mammalia; Eutheria; Rodentia;
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 AND 2 (S
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED
                                                                   PARAXIAL MESODERM SUBUNIT: CAN BIND (PROBABLE).
                                                                                              FUNCTION: INHIBITS PRIMARY NEUROGENESIS. MAY BE REQUIRED TO DIVERT NEURONS ALONG A SPECIFIC DIFFERENTIATION PATHWAY. PLAY A ROLE IN THE FORMATION OF SOMITE BOUNDARIES DURING SEGMENTATION OF THE
       DOMAIN:
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                   AND PARAXIAL MESODERM DURING EMBRYOGENESIS
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nite boundaries.";
19:274-278(1998).
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        DOMAIN IS REQUIRED
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SMART; SM00181; EGF; 6.
PROSITE; PS00022; EGF_1; 6.
PROSITE; PS01186; EGF_2; 6.
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                 CR--IXNQKCFQHLDDCCSXXCNXXNXCV 27
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IPR000742;
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IPR001438;
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Pred. No. 4.1;
1; Mismatches
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EGF-LIKE
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use by non-profit institutions as long
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                                                              InterPro;
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EMBL;
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                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                    MIM;
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MEDLINE=20206573; P
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Mammalia; Eutheria;
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                 SMART;
                               PRINTS;
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                                                                                                                                                                                                                                                                                                                        EMBL;
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15-JUN-2002
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SUBUNIT: CAN BIND AND ACTIVATE NOTCH-1 OR ANOTHER NOTCH RECEPTOR (BY SIMILARITY).
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                                                                                                                                    277300; -
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AF241371;
AF241371;
AF241372;
BC000218;
                                                                                                                                                                P00740; 1EDM;
HGNC:2909; I
                                                                                                                                                                                                                                                                                    AF241373; AAF62542.1;
AF241367; AAF62542.1;
AF241368; AAF62542.1;
                 SM00181; EGF;
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PS00022;
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                                                              IPR001438;
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IPR000742;
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                                                                                                                                                                                                                                                    AAF62542.1;
AAF62542.1;
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                                                                                                                                                                                                                       AAF62542
                               EGFBLOOD.
                                                                                                                                                                    DLL3
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EGF_1; 6
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Primates;
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EGF_2.
EGF_Ca.
EGF_II.
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Q99466; 000306;
15-JUN-2002 (Rel
                                              Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Nakamura Y., Ando A., Inoko H., Ikemura T., Mita "Gene organization of human NOTCH4 and (CTG)n pol human counterpart gene of mouse proto-oncogene In Gene 189:235-244(1997).
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SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND TISSUE-Bone marrow, and Heart; MEDLINE=98360091; PubMed-9693032;
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Mammalia; Eutheria;
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MEDLINE=97311416; PubMed=9168133;
                                                                                                                                               SEQUENCE FROM N.A.
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Signal; EGF-like
Differentiation;
                                                                                                                                                                                                                                                                      15-JUN-2002
15-JUN-2002
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EGF-LIKE 1.

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BY SIMILARITY

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DELTA-LIKE PROTEIN 3

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CYTOPLASMIC (POTENT)
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l; Mismatches
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Catarrhini;
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                                                                                                                                               POLYMORPHISM
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Q9UII9;
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e Int3.";
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proteclytical processing NICD is translocated to the nucleus.

-!- ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; may be produced by alternative splicing.

-!- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in the lung and placenta and at low levels in the liver, skeletal muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow and fetal liver. No expression was seen in adult brain or peripheral blood leukocytes.

-!- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentin dependent gamma-secretase to release a notch-h-derived nontial containing the intermediate fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gray G.E., Mann R.S., Mitsiadis E., Hen. Banks A., Leiman J., Ward D., Ish-Horow. "Human ligands of the Notch receptor."; Am. J. Pathol. 154:785-794(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-503 FROM N.A., AND VARIANTS Miyagawa T., Tokunaga K., Hojho H.; "Human notch4 gene variant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Friedman C., Chen L., Trask B.J., Sp "Cloning, characterization, and the sequence of the human NOTCH4 gene."; Genomics 51:45-58(1998).
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Gray G.E., Mann R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li L., Huang G.M., Banta A.B., Deng Y., Friedman C., Chen L., Trask B.J., Spies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and
peptide) is polymorphic and the number of population (from 6 to 12).

SIMILARITY: BELONGS TO THE NOTCH FAMILY. SIMILARITY: CONTAINS 28 EGF-LIKE DOMAINS. SIMILARITY: CONTAINS 3 LIN/MOTCH REPEATS. SIMILARITY: CONTAINS 3 LIN/MOTCH REPEATS. CAUTION: Ref. 1 sequence differs from that
                                                                                                                                                                                                                                                                                                             notch-derived peptide containing the intracellular domain (from the membrane (Bv similarit...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  terminal fragment N(EC) which are probably lind bonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptotic programs. May regulate branching morphogenesis developing vascular system (By similarity).

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a terminal fragment N(EC) which are probably linked by dist
                                                                                                                                                                                                                                  POLYMORPHISM: The poly-Leu region
                                                                                                                                                                                                                                                                      from the membrane (By similarity).

PTM: Phosphorylated (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitsiadis E., Henrique D., Carcangiu M.-L.,
Ward D., Ish-Horowitz D., Artavanis-Tsakonas
                                                                                                                                                                                                                               (By similarity).
oly-Leu region of NOTCH4 (in the signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ
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T., Rowen
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56.8-kilobase
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requires a license agreement (See ) equires a license agreement (S email to license@isb-sib.ch). BAA09708.1; ALT\_FRAME. BAA13116.1; -. AAC32288.1; -. There are no rest http://www.isb-sib.ch/announce/ Usage and through the bу restrictions and EMBL for collaboration -9 on

CAUTION: Ref.1 se in position 1438

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SM00019; EGF_CA; 11.
SM00001; EGF_LIKe; 15.
SM000004; NL; 2.
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P08709; 1E
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E; PS50297; ANK_REP_REGION; 1.
E; PS00010; ASX_HYDROXYL; 11.
E; PS00022; EGF 1; 28.
E; PS01186; EGF_2; 21.
E; PS01187; EGF_CA; 9.
EFF_CA; 9.
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IPR000742;
IPR001881;
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EGF_2.
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Notch.
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EXYRAGELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

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EGF-LIKE 3.

EGF-LIKE 5. CALCIUM-BINDING

EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 10.

EGF-LIKE 10.

EGF-LIKE 11.

CALCIUM-BINDING

EGF-LIKE 11.

CALCIUM-BINDING

EGF-LIKE 12.

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EGF-LIKE 13.

CALCIUM-BINDING

EGF-LIKE 15.

CALCIUM-BINDING

EGF-LIKE 16.

EGF-LIKE 17.

EGF-LIKE 18.

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EGF-LIKE 24.

EGF-LIKE 25.

EGF-LIKE 26.

EGF-LIKE 27.

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EGF-LIKE 28.

EGF-LIKE 28.

EGF-LIKE 29.

POLY-ARG.

LIN/NOTCH 1.

LIN/NOTCH 3.
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                                                                   SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2) STRAIN-CD-1; TISSUE-Embryo; MEDLINE-93050801; PubMed-1426644; Reaume A.G., Conlon R.A., Zirngibl R., Yan "Expression analysis of a Notch homologue Dev. Biol. 154:377-387(1992).
                                                                                                                                                                     Genomics
                                                                                                                                                                                  Franco del Amo F., Gendron-Maguire N
Copeland N.G., Gridley T.;
"Cloning, analysis, and chromosomal
homolog of Drosophila Notch.";
Genomics 15:259-264(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                  NTC1_MOUSE STANDARD; PRT; 2531 AA (201705; Q90M58; Q99JC2; Q06007; Q61905; Q9R (01-FEB-1995 (Rel. 32, Created) (1-FEB-1996 (Rel. 33, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat. Neurogenic locus notch homolog protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 protein 1 prote
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Eukaryota; Metazoa; (
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                    SEQUENCE OF 1551-1647 TISSUE-Embryo;
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     MEDLINE-93048835; PubMed-1425352
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MEDLINE=93194170; PubMed=8449489;
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NOTCH1 OR MOTCH
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protein 1 precursor (Notch
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"Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
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                                                                                                                    <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POST-TRANSLATIONAL PROCESSING. MEDLINE=21374376; PubMed=11459941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc.
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[7]
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MEDLINE=93178563; PubMed=8440332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem.
                                                                                                                                                                                                                                                                      FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation. May be involved in mesoderm development, somite formation and neurogeness. Involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induction
                 proteolytical processing NICD is translocated to the ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and produced by alternative splicing.
TISSUE SPECIFICITY: Highly expressed in the brain, luthymus. Expressed at lower levels in the spleen, bone spinal cord, eyes, mammary gland, liver, intestine, s
                                                                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein. Following
                                                                                                                                                                                                           maturation of both CD4+ and CD8+ cells in the thymus. SUBUNIT: Heterodimer of a C-terminal fragment N(TM) a terminal fragment N(EC) which are probably linked by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lett. 455:276-280(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of HES-1 in a mouse T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schroeter E.H., Mumm J.S., Kopan R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lendahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276:40268-40273(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is cleaved constitutively by a furin-like
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mammary
heart.
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a mouse homolog of Drosophila Notch,
early postimplantation mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95:8108-8112(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed activation of the Notch1 T lymphoma cell line, DL-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FURIN-LIKE CONVERTASE,
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              bone-marrow,
ne, skeletal
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                                                                lung
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                                                                                                          nucleus.
2; may b
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SIMILARITY: BELONGS TO THE NOTCH FA
SIMILARITY: CONTAINS 36 EGF-LIKE DC
SIMILARITY: CONTAINS 3 LIN/NOTCH RE
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called neth over the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the convertion of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     notch-derived peptide containing the intracellular domain (NICD)
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PTM: Synt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which
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Synthesized in the endoplasmic reticulum as an inactive form
h is proteolytically cleaved by a furin-like convertase in th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the membrane.
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This entities requires a license agreement (S or send an email to license@isb-sib.ch). use by non-profit institutions a modified and this statement is not the between European SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its institutions as long as its content removed. (See http://www.isb-sib. Usage уd and for .ch/announce/ in no way

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HSSP; P00/40,
MGD; MGI:97363; Notc....
InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000761; EGF-like.
InterPro; IPR000742; EGF-2.
InterPro; IPR0001438; EGF-[II.
                                                                                                                                                                                                                Pfam; PF00023; ank; 7.

Pfam; PF00026; notch; 3.

Pfam; PF00066; notch; 3.

Pfam; PF00066; notch; 3.

Pfam; PF00010; EGFELOOD.

PRINTS; PR00110; EGF_LOOD.

PRINTS; PR00179; EGF_CA; 23.

SMART; SM00001; EGF_11ke; 11

SMART; SM00004; NL; 2.

PROSITE; PS5008; ANK_REPEAT; PROSITE; PS5008; ANK_REPEAT; PROSITE; PS50010; ASX_HYDROX: PROSITE; PS00110; ASX_HYDROX: PROSITE; PS001187; EGF_CA; 21

PROSITE; PS01187; EGF_CA; 21
CHAIN
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EMBL;
EMBL;
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                                                                                                                                    SIGNAL
                                                                                                                                                                                Developmental protein;
                                                                                                                                                                                                     Receptor;
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                                                                                                                                                           Transcription regulation; Activator; Differentiation; intal protein; Repeat; ANK repeat; EGF-like domain; rane; Glycoprotein; Signal; Phosphorylation;
                                                                               1711
1744
                                                                                                                                                  splicing
                                                                                                                                                                                                                ; ANK_REPEAT; 2.
; ANK_REP_REGION; 1.
; ANK_REP_REGION; 1.
; ASX_HYDROXYL; 22.
; EGF_1; 34.
; EGF_2; 27.
; EGF_2; 27.
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99
                            EXTRACELLULAR POTENTIAL.
CYTOPLASMIC (P.
EGF-LIKE
                                                                                 NOTCH
                                                                                                                NEUROGENIC LOCUS
                                                                               EXTRACELLULAR TRUNCATION INTRACELLULAR DOMAIN.
                                                               (POTENTIAL)
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PROTEIN

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RESULT
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DOMAIN
            TISSUE SPECIFICITY.
MEDLINE=93002015; PubMed=1295745;
Weinmaster G., Roberts V.J., Lemke
"Notch2: a second mammalian Notch
Development 116:931-941(1992).
                                                                                                                                                        Weinmaster G., Roberts V.J., Lemke G.;
"A homolog of Drosophila Notch expressed development.";
                                                                                                                                                                              TISSUE-Schwann cel
MEDLINE-92111383;
                                                                                                                                                                                                                                                        Q07008;
01-NOV-1995 (Rel. 32,
15-JUL-1999 (Rel. 38,
15-JUN-2002 (Rel. 41)
TISSUE
                                                                 neural
                                                                        "Notch1 and Notch3 instructively restrict
                                                                                      Tanigaki K.,
                                                                                              MEDLINE-21094508;
                                                                                                       FUNCTION
                                                                                                                     Submitted
                                                                                                                                    REVISIONS
                                                                                                                                                  Development 113:199-205(1991).
                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                           Neurogenic
NOTCH1.
                                                                                                                                                                                                                                                                                       NTC1_RAT
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                                                         progenitor cells
29:45-55(2001).
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8; Conserv
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                                                                                                                    (APR-1998) to
                                                                                                                             G
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                                                                                       Nogaki
                                                                                                                                   1652-1653
                                                                                                                                                                                      cell;
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                  notch
                                                                                      PubMed=11182080;
ki F., Takahashi
                                                                                                                                                                      PubMed=1764995;
berts V.J., Lemke G.;
                                                                                                                                                                                                                                                                                                                                                                                      36
                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                       Created)
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                                                                                                                    the EMBL/GenBank/DDBJ
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                             Lemke
                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                astroglial fate.";
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                otation update)
protein 1 precursor
                                                                                      ū,
                   gene.";
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                                                                                                                     databases
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                                                                                       Kurooka
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development.";
J. Comp. Neuro
-1- FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). Acts instructively to control the cell fate determination of CNS multipotent progenitor cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              terminal fragment N(EC) which are probably linbonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
proteolytical processing NICD is translocated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed in postnatal central nervous system (CNS) germinal zo and, in early postnatal life, within numerous cells throughout CNS. Found in both subventricular and ventricular germinal zone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteolytical processing similarity).
TISSUE SPECIFICITY: Expre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               suppression.
SUBUNIT: Heterodimer of a C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resulting in astroglial induction and neuron/oligodendrocyte
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This entities requires a license agreement or send an email to license@isb-sib.cl use by non-profit institutions as long modified and this statement is not removed. between the Swiss Institute of Bioinf the European Bioinformatics Institute SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation email to license@isb-sib.ch) (See http://www.isb-sib There as its content is in Usage γď and for in no way commercial

notch-derived peptide containing the intracellular domain (from the membrane (By similarity).

-! PTM: Phosphorylated (By similarity).
-! SIMILARITY: BELONGS TO THE NOTCH FAMILY.
-! SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
-! SIMILARITY: CONTAINS 5 ANK REPEATS.

PTM: Synthesized in the endoplasmic reticulum as an inactive which is proteolytically cleaved by a furin-like convertage trans-Golgi network before it reaches the plasma membrane to an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment cotch extracellular truncation (NEXT). This fragment is then cleaved by presentin dependent gamma-secretase to release a cleaved by presentin dependent gamma-secretase to release

an inactive form convertase in the membrane to yield

Following

called

levels

adult days 12 and

Pfam; PF00023; ank; 6.

Pfam; PF00066; notch; 3.

PRINTS; PR00010; EGFPT PRINTS; PR00011 InterPro; InterPro; EMBL; HSSP; InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; X57405; P00740; SM00248; SM00179; SM00001; PR00011; EGFLAMININ PR01452; NOTCH. IPR001881; IPR001438; IPR002049; IPR000800; IPR000742; 740; 1EDM. IPR002110; ANK. IPR000561; IPR000152; CAA40667.1; ANK; 5. EGF\_CA; 25. EGF\_like; 10. EGFBLOOD. . 6. . Asx\_hydroxyl.
EGF-like.
EGF\_2.
EGF\_Ca.
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PROSITE; PS50088; ANK_REPEAR; 4.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS000102; EGF_1; 35.

PROSITE; PS01186; EGF_2; 26.

PROSITE; PS01187; EGF_CA; 21.

Receptor; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Romenumitar
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CYTOPLASMIC (POTENTIAL).

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EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10.

EGF-LIKE 11.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13.

EGF-LIKE 14.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 16.

EGF-LIKE 17.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 18.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 22.

EGF-LIKE 23.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 24.

EGF-LIKE 25.

CALCIUM-BINDING (POTENTIAL).

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EGF-LIKE 27.

CALCIUM-BINDING (POTENTIAL).

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EGF-LIKE 32.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 33.

EGF-LIKE 34.

EGF-LIKE 35.

EGF-LIKE 36.

EGF-LIKE 37.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 38.

EGF-LIKE 39.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 39.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 39.

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042374 PRELIMINARY; PRT; 752 AA.
042374; PREMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NOTCH 2 OR NOTCH6.

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PRINTS; PRO0011; EGFLAMININ.

SMART; SM00051; DSL; 1.

SMART; SM00179; EGF_CA; 4.

SMART; SM00101; EGF_1ike; 4.

SMART; SM00001; EGF_1ike; 4.

SMART; SM00001; EGF_1; UNKNOWN_B.

PROSITE; PS00012; EGF_1; UNKNOWN_B.

PROSITE; PS01186; EGF_2; 8.

PROSITE; PS01187; EGF_CA; 2.
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PROSITE; PS00022; EGF_1; UNKNOWN_17.
PROSITE; PS01186; EGF_2; 15.
PROSITE; PS01187; EGF_CA; 7.
Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20054100; PubMed=10585570; Smithers L.E., Haddon C., Jiang Y.-
"Sequence and embryonic expression Mech. Dev. 90:119-123(2000).
EMBL; AF146429; AAF27299.1; -.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00008; EGF;
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9; Conserv
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IPR000561;
IPR000742;
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752 AA;
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                                                                                                                                                                                                                                                                                                                                                      AA,
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A; 72547 MW; 0AD6C34C8579116B
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82103 MW;
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EGF_2.
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34.5%;
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Last annotation update)
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                                                                                                                                                                                                                                                            Score 55;
Pred. No.
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Pred. No.
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01-MAY-2000
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P79941;
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Q9U4A2;
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InterPro;
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01-DEC-2001
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Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 8.
Pfam; PF0000010; EGFBLOOD.
SMART; SM00051; DSL; 1.
SMART; SM00001; EGF_CA; 3.
SMART; SM00001; EGF_like; 5.
PROSITE; PS00010; ASX_HYDROXYL; UN
                                                                                                                                                                                                                                    mesoderm in Xenopus embryos."; ""GULACES SEGMENTATION OF SUBMITTED (SEP-1996) to the EMBL/GenBank/DDBJ databases EMBL; U70843; AAB37131.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerebral malaria.";
Proc. Natl. Acad. Sci. U.S.A.
EMBL; AF193424; AAF18980.1; -
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Pinches R., Baruch D.I., Newbold C.I., Miller L.H.;
"Identification of a Plasmodium falciparum intercellu
molecule-1 binding domain: A parasite adhesion trait
                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00605; ATPASE_C; NON_TER 1685 1685
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h ligand X-delta-2.
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9; Conserv
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; IPR000561; EGF-11ke.
; IPR000742; EGF_2:
; IPR001481; EGF_Ca.
; IPR001438; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                          Batrachia; Anura; Mesobatrachia; ae; Xenopus.
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                                                                                                                                                                                                                      IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                         Wettstein D.A., Chitnis A.B., n ligand, X-Delta-2, mediates
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EGF_1; UNKNOWN_8
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D1FD426666B0551E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
2.6;
                                                                                                                                                                                                                                                                                                                            Kintner
                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata;
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۲.
                                                                                                                                                                                                                                                                                                                                                                                                            Pipoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kyes
                                                                                                                                                                                                                                                                                                                                                                                                            Pipidae;
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Miyatani

Euteleostomi;

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Xenopus

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Best Local S
Matches 10
                                                                                              Query Match
Best Local :
                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSULLO,
PROSITE; PSULL87; EGF
Calclum-binding; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O13149 PRELIMINARY;
O13149;
O1-JUL-1997 (TIEMBLIEL 0
01-JUL-1997 (TIEMBLIEL 0
01-MAR 2002 (TIEMBLIEL 2
                                                                                                                                                                                                                                                                                             PRINTS; PRO0010; I
PRINTS; PRO0011; I
PRINTS; PRO0011; I
PRINTS; PRO00124; AL
SMART; SM00248; AL
SMART; SM00001; EC
SMART; SM00001; EC
SMART; SM00004; NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu Eukaryota, Metazoa, Chordata, Craniata, Verte Actinopterygii; Neopterygii; Teleostei; Eutel Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae, Takifugu.
                                                                                                                                                                                                   PROSITE; PS5008B; ANK REPEAT; 8.

PROSITE; PS50297; ANK_REP_REGION; 2.

PROSITE; PS00010; ASX_HYDROXYL; 22.

PROSITE; PS00022; EGF_1; UNKNOWN_35.

PROSITE; PS01187; EGF_2; 29.

PROSITE; PS01187; EGF_CA; 20.
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of Fugu Notch submitted (JUN-1997) to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Notch 2 (Fragment).
                                                                                                                                                                      Hydroxylation; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                    290 CSENIDDCDTAACSPGSTCV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CR--IXNOKCFOHLDDCCSXXCNXXNXCV 27
                                                CFQHLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRPGFSGPRCELNIDDCASSPCANGGTCV 440
                                                                                                                                                                                                                                                                                                                                                                                                         PF00066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB004829;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00023;
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                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 34.10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000152;
IPR000561;
IPR000742;
IPR001881;
IPR001438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002
                                                                                                                                           2447
                                                                                                                                                                                   01187; EGF_CA; 20 Calcium-binding;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trowsdale J.;
                                                                                                                                                                                                                                                                                                                                                                                                                       EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1EDM.
                                                                                                                                                                                                                                                                                            ANK; 5.
; EGF_CA; 20.
; EGF_like; 14.
; NL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                       notch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; EGF_2; 7.

7; EGF_CA; 2.

;; EGF-like domain; G

70667 MW; D7DK
                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                                                         EGFLAMININ.
FNTYPEI.
                                                                                                                                                                                                                                                                                                                                                                                         EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                       35.
                                                                                             37.1%;
35.0%;
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Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asx_hydroxyl
EGF-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notch
                                                                                                                                           262541 MW;
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04, Last sequence update)
20, Last annotation update)
                                                                                                                                                                        ing; EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene.";
                                                 27
                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.6
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; 1
Pred. No. 1
                                                                                              Pred.
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                                                                              Mismatches
                                                                                                                                          1A8E2A372A085D84 CRC64;
                                                                                                           52;
                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Takifugu
                                                                                                                                                                                     domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         рв
1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kifugu rubripes).
  Vertebrata; Euteleostomi;
  Euteleostei; Neoteleostei;
                                                                                                           DΒ
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                                                                                                           13;
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                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                        Length 2447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 642;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                             0,
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                                                                             Gaps
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                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
RESULT
Q90YD2
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                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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Best Local S
Matches 7
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EMBL; AB027537; BAB59049.1; -.

InterPro; IPR000152; Asx_hydroxy1.

InterPro; IPR001774; DSL.

InterPro; IPR000742; EGF-1ike.

InterPro; IPR000742; EGF_2.

InterPro; IPR0001801; EGF_Ca.

InterPro; IPR001007; VWF_C.

Pfam; PF001414; DSL; 1.

Pfam; PF00008; EGF; 14.
                                                                                                                                                                                                                                                                          01-MAR-2001
01-JUN-2002
CG8023 prote
        MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q90YD2;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                               CG8023
                                                                                                                                                                                                                                                                                                                                          Q9VSG1;
                                                                                                                                                                                                                                                                                                                                                       Q9VSG1
   Ballew
                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                         01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "X-Serrate-1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q90YD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinoshita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiyota T., Jono H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=21541033; PubMed=11685570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-SERRATE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                   622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       x-Serrate-1 is involved in primary neurogenesis
complementary manner with X-Delta-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CHENINDCESNPCNNGGTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFQHLDDCCSXXCNXXNXCV
                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laevis (African clawed
ta; Metazoa; Chordata; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P$00010; ASX_HYDROXYL; UNKNOWN_10.
P$00022; EGF_1; UNKNOWN_11.
P$01186; EGF_2; UNKNOWN_12.
P$01187; EGF_CA; UNKNOWN_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Batrachia; Anura;
ae; Xenopus.
                                                                                                                                                                                                                                                                                       ) (TrEMBLrel.
| (TrEMBLrel.
| TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211:367-376(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuriyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133807 MW;
Baxendale
                                                                                                                                                                                                                                                                                        13,
16,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19,
19,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                   641
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.1,
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d frog).
Craniata;
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A9C09C420CC157C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hasegawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1214
                                                                                                                                                                                                                                                                                                                                                      244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB
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                                                                                                                                                                                                                          Hexapoda;
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Insecta;

Length 1214;

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Best Local S
Matches 8
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01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
                     investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XV21
                                                                                            none;
                                                                                                                 MEDLINE-99069613;
                                                                                                                                       SEQUENCE FROM N.A.
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                                                "Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0035860; CG8023.
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281540;
                                                                                                                                                                                                                                                                                                                                                                                              protein.
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;; PS00813; IF4E; 1.
E 244 AA; 28492 MW; 2
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8; Conserv
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                                                                                                                 PubMed=9851916;
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Last annotation update)
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Pred. No. 1.4;
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RESULT
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Matches 9
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InterPro; IPR000151; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR000800; Notch.
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01-NOV-1996
01-DEC-2001
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InterPro;
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SMART; SM00274; FOLN; 6.
SEQUENCE 354 AA; 37229 MW;
                              SMART;
                                         PRINTS; PRO0010; EGFBLOOD.
PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 4.
SMART; SM000179; EGF_CA; 24.
SMART; SM00001; EGF_Like; 11
                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Scalloped wings is the Lucilia cuprina Notch homologue and a candidate for the modifier of fitness and asymmetry of diazinon resistance.";
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Pterygota; Neoptera; Endopi
Oestroidea; Calliphoridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen Z., Newsome T., Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96400928; PubMed=8807304; Davies A.G., Game A.Y., Chen Z., McKenzie J.A., Batterham P.;
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                                                                                                                                                       Pfam;
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                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                        Chen Z., McKenzie J.A., Batterham
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SS SEEKING;
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[2]
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PF00008; EGF; 36.
PF00066; notch; 3.
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                                SM00001;
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9; Conserv
PS50088; ANK_REPEAT; 5. PS50297; ANK_REP_REGION;
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IPR003645;
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                              NL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    McKenzie J.A., Batterham P.;
to the EMBL/GenBank/DDBJ databases.
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Pred. No.
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                            Q91902
Q91902;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
Q1-DEC-2001
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Q9LP17;
Q9LP17;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
                                                                                                                                                                                     Eukaryota; Metazoa; C
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
Ecker J.R.;
                                       SEQUENCE FROM N.A. MEDLINE-95319507;
                                                                                                                            Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Kl
Chao P., Altafi H., Bei Q., Chin C., Chiou J., Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00010; ASX_HYDROXYL; 22.
PROSITE; PS00022; ECF_1; UNKNOWN_34.
PROSITE; PS01186; ECF_2; 28.
PROSITE; PS01187; ECF_CA; 21.
ANK repeat; Calcium-binding; EGF-1ike domain; Glycoprotein; Hydroxylation; Repeat.
SEQUENCE 2653 AA; 285928 MW; 6AF2A058FEEC6329 CRC64;
            Henrique
                                                                                                                                                                                                                                                                             X-delta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2001) to the EMBL; AC017118; AAF25976.1; InterPro; IPR003441; NAM. Pfam; PF02365; NAM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic sequence for Arabidopsis thaliana
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7; Conservative
                                                                                                                                                                                                                                                                                               (TrEMBLrel.) (TrEMBLrel.)
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0 (TrEMBLrel. 15,
1 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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               Adam
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            PubMed=7596411;
J., Myat A., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41520 MW;
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         Myat A.,
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, Last sequence upo
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                                                                                                                                                                                                                                                                                               Created)
Last sequence up
Last annotation
                                                                                                                                                                                  Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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1; Mismatches
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         Chitnis
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            Α.,
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      J.,
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oi E., Con
         Ish-Horowicz
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Lee J.,
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InterPro;
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[2]
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Smye R.;
Submitted (MAR-1998) to the EMBL/CULLERBL; 269792; CAA93668.2; -
EMBL; AL022270; CAA93668.2; JOINED.
R EMBL; AL022270; CAB63434.1; -
R EMBL; 269792; CAB63434.1; JOINED.
NR HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00051; DSL; 1.

SMART; SM00079; EGF_CA; 4.

SMART; SM00001; EGF_Like; 4.

PROSITE; PS00010; ASX_HYDROXYI

PROSITE; PS00022; EGF_1; UNKNN

PROSITE; PS01186; EGF_2; 8.
                                                                                                                                                     "Genome sequence of the nema investigating biology."; science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX_HYDROXYL; UN
PROSITE; PS00022; EGF_1; UNKNOWN_8
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01187; EGF_CA; 2.
Calcium-binding; EGF-like domain;
SEQUENCE 721 AA; 79922 MW; 9EB
                                                                                                                                                                                                              SEQUENCE FROM N.A MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95319503; PubMed-7596407; Chitnis A., Henrique D., Lewis J., Ish-Hc "Primary neurogenesis in Xenopus embryos the Drosophila neurogenic gene Delta."; Nature 375.761-766(1995).
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01-JUN-2002
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InterPro;
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                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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PF00008; EGF;
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8; Conserv
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IPR000742;
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                                                                                                                                                                                                              PubMed=9851916;
                                                                                                                                                                                                                                                                                                                               Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF_like.
EGF_2.
EGF_Ca.
EGF_II.
                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.0%;
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                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                       01,
13,
21,
                                                                                                                                                                                   nematode
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                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence
Last annotation
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                                                                                              EMBL/GenBank/DDBJ
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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9EBDC85C439DD194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_3.
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                                                                                                                                                                                                                                                                                                                                                                                                     sequence up
annotation
                                                                                                                                                                                   G
                                                                                                                                                                                  elegans:
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No.
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ion update)
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CRC64;
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by a homologue of
                                                                                                                                                                                  for
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Best Local S
Matches 7
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PROSITE; PS01225; CTG
PROSITE; PS01022; EGF
PROSITE; PS01186; EGF
PROSITE; PS01187; EGGE
Calclum-binding; EGF
SEQUENCE 1440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0010; I
PRINTS; PRO0019; I
SMART; SM00041; C'
SMART; SM00179; EC
SMART; SM00001; EC
InterPro;
Pfam; PF0
                                                                                                                                                                                                                                                                                                                                                        061240; PRELIMINARY;
061240; O1-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                              InterPro;
InterPro;
                                                                                                                                                                                                                                                          Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
NCBI_TaxID=7729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
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                                                                                                                               HSSP; P00740; 1EDM
                                                                                                                                                             Hori S., Saitoh T., Matsumoto M., Mak
"Notch homologue from Halocynthia rot
in the central nervous system during
Dev. Genes Evol. 207:371-380(1997).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                HRNOTCH
                                                                                                                                                                                                                                                                                                                                          HrNotch protein.
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                                                                InterPro;
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                                                                                                                                              Genes Evol. 207:371-38; AB001327; BAA25571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEKNIDDCVNSKCENGGKCV 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00054; laminin_G; 1.
PF00560; LRR; 18.
PF01463; LRRCT; 4.
PF01462; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00282;
SM00370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00369;
        ; IPR002110; ANK.
); IPR000152; Asx_hydroxyl.
); IPR0007561; EGF-like.
); IPR000742; EGF_2.
0; IPR001881; EGF_Ca.
0; IPR001438; EGF_II.
0; IPR000800; Notch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M00369; LRR_TYP; 7.

PS001010; ASX_HYDROXYL; UNKNOWN_1.

PS01225; CTCK_2; 1.

PS001225; EGF_1; UNKNOWN_7.

PS01186; EGF_2; 5.

PS01187; EGF_CA; 1.

binding; EGF_1ke domain; Glycoprotein; Repeat.

binding; EGF-1ke domain; GB5D198645D73670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001438;
IPR001791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; LRRCT; 4.
3; LRRNT; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF_CA; 2.
EGF_like; 5.
EGF_like; 5.
LamG; 1.
LRR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CT;
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EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.0%;
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                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                              Makabe K.W., Nishida H.;
roretzi is preferentially expressed
ing ascidian embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                             2352
                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                Ascidiacea;
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Best Local
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                                                              SMART; SMO0001; EGF_like; 4.

PROSITE; PS00101; ASX_MYDROXYL; 3

PROSITE; PS01180; CUB; 27.

PROSITE; PS00102; EGF_l; UNKNOWN_
PROSITE; PS01186; EGF_l; 2.

PROSITE; PS01187; EGF_CA; 4.

Calcium-binding; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PE00008; EGF; 32.
Pfam; PF00066; notch; 3.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM0024B; ANK; 5.
SMART; SM00179; EGF_CA; 17.
SMART; SM00001; EGF_Like; 9.
SMART; SM00004; NL; 2.
                                                                                                                                                                                                                                             Interpro; IPR000152; A Interpro; IPR000859; C Interpro; IPR000561; E Interpro; IPR000742; E Interpro; IPR001881; E
                                                                                                                                                               SMART; SM00042; (SMART; SM00179; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Cr
01-JAN-1999 (TrEMBLrel. 09, La
01-JUN-2002 (TrEMBLrel. 21, La
Intrinsic factor-B12 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                          "The intrinsic factor-vitamin B12 receptor antibodies is a megalin-binding peripheral homology to developmental proteins.", Biol. Chem. 273:5235-5242(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       070244;
                                                                                                                                                                                                              Pfam; PF000431; CUB; 27. Pfam; PF00008; EGF; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98148073; PubMed=9478979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070244
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   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANK repeat; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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E; PS50297; ANK_REP_REGION; 1.
E; PS000101; ASX_HYDROXYL; 18.
E; PS00022; EGF_1; UNKNOWN_28.
E; PS01186; EGF_2; 22.
E; PS01187; EGF_CA; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                   Repeat; Signal.
   21
3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat
                                                                                                                                                                                CUB; 26.
EGF_CA; 4.
   Ä,
                                                                                                                                                                                                                                                                                                                                                 AAC71661.1;
                  3623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                             Asx_hydroxyl.
CUB_domain.
EGF-like.
EGF_2.
EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252623 MW;
   20 POTENTIAL.
23 INTRINSIC FACTOR-B12
398981 MW; 39FB792AC6545240
                                                                                                                 UNKNOWN_4
                                                                                                                                                                                                                                                                                                                                                             26 CUB DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
                                                                  domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kristiansen |
Pontillon F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13DB1C056BB0D08D
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da F.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2352;
                                                                  Hydroxylation;
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   RECEPTOR.
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J.H., Christensen E.I.,

Rattus

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Gaps

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j

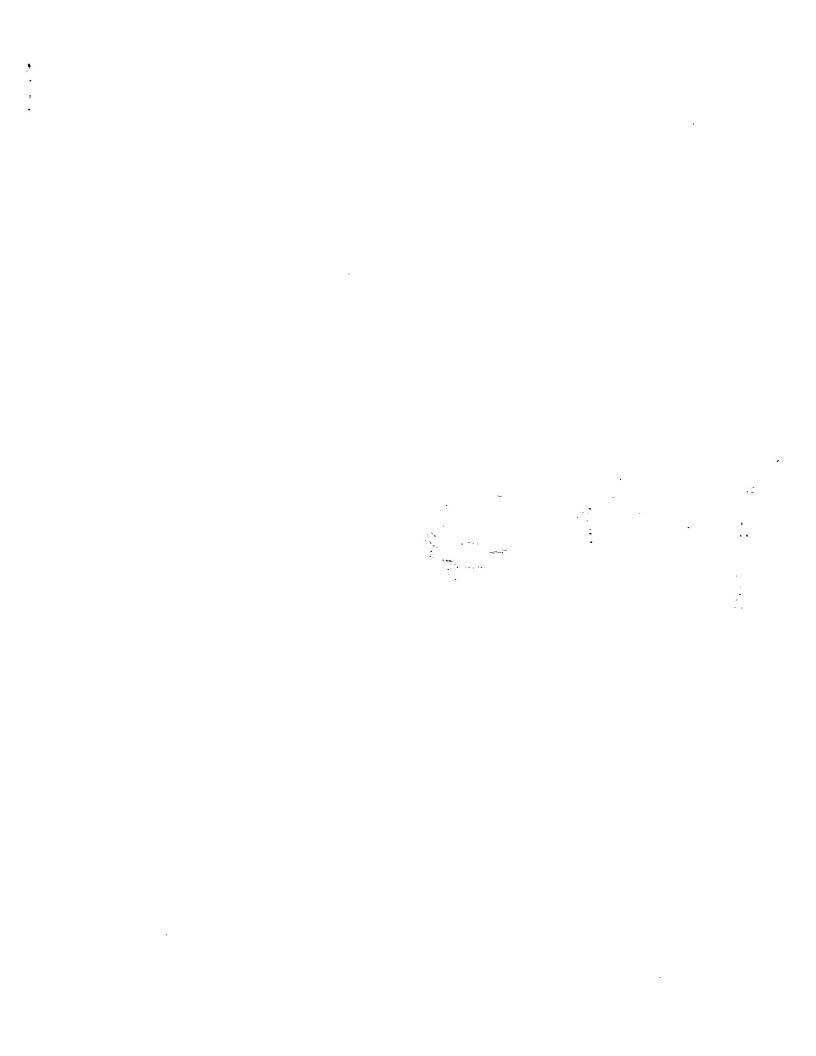
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RESULT 15
Q23456
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Search completed: January 14, 2003, 18:29:05 Job time: 32 secs
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                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q23456
Q23456
Q23456;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2K287.4 protein.
                                                                                                                                                                       InterPro; IPRO02223; Kunitz_BPTI.
InterPro; IPRO02299; WR1/EB.
Pfam; PP00014; Kunitz_BPTI; 7.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 6.
SMART; SM00131; KU; 7.
SMART; SM00139; WR1; 3.
PROSITE; PS0279; BPTI_KUNITZ_2; 7.
Serine Protease inhibitor.
Serine Protease inhibitor.
Serine Protease 1208 AA; 133055 MW; F5BABF7D81BDB229 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.

Cukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
EMBL; 270757; CAA64800.1; -.
HSSP; P31713; 1SHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MCMUTTAY A.A.;

Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 ONCTENINDCSSNPCLNGGTCI 448
                                                         805 NONNEQSEDS-CSRACGATIVE 825
                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QKCFQHLDDCCSXXCNXXNXCV
                                                                               5 NQKCFQHLDDCCSXXCNXXNXC 26
                                                                                                                34.6%; Score 48.5; liarity 45.5%; Pred. No. 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 3623;
                                                                                                                                              DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                  11;
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                                                                                                                  ۲,
                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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## Sequence Family Search of Proteins (/sqsfp)

In the sequence family search, each amino acid in the query has to match either the exact amino acid or a family member equivalent, as shown in the Family Equivalence Table below. The Family Equivalence Table is applied only to each common amino acid in the sequence. Specific uncommon amino acids may be included in the sequence; however, family equivalents only exist for the common amino acids. An amino acid family is based on a conservative substitution of amino acids sharing a similar chemical property. Each common amino acid in the query is converted to its family class members in a search. A match occurs on a query sequence if each amino acid is exactly matched or any of its family members are encountered. For example, the Hydrophobic-Aromatic family consists of the common amino acids F, W, and Y. If the amino acid F is specified within a sequence exact family search, it will match on amino acids F, W, or Y.

## FAMILY EQUIVALENCE TABLE

Family Class Name	Family Class Members				
Neutral-Weakly Hydrophobic	Ala (A), Gly (G), Pro (P), Ser (S), Thr (T)				
Hydrophilic-Acid Amine	Asn (N), Asp (D), Gln (Q), Glu (E)				
Hydrophilic-Basic	Arg (R), His (H), Lys (K)				
Hydrophobic	Ile (I), Met (M), Leu (L), Val (V)				
Hydrophobic-Aromatic	Phe (F), Trp (W), Tyr (Y)				
Crosslinking	Cys (C)				

		ı	ı

family search -

conservative substitution

=> fil req; d que 12 FILE 'REGISTRY' ENTERED AT 08:39:59 ON 15 JAN 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELP USAGETERMS" FOR DETAILS. COPYRIGHT (C) 2003 American Chemical Society (ACS)

Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 14 JAN 2003 HIGHEST RN 479024-64-1 DICTIONARY FILE UPDATES: 14 JAN 2003 HIGHEST RN 479024-64-1

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details: http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

L2 12 SEA FILE=REGISTRY ABB=ON CRI'HYP'NQKCFQHLDDCCS/SQSFP /

=> d rn cn sql kwic nte 12 1-12; fil capl; s 12

L2ANSWER 1 OF 12 REGISTRY COPYRIGHT 2003 ACS

332843-22-8) REGISTRY - Wee registry # to match sequence to citation - CA reference # 3
Peptide, (Cys-Arg-Ile-Xaa-Asn-Gln-Lys-Cys-Phe-Gln-His-Leu-Asp-Asp-Cys-Cys-RN CN

Ser-Xaa-Xaa-Cys-Asn-Xaa-Xaa-Asn-Xaa-Cys-Val) (9CI) (CA INDEX NAME)

27 SQL SEO

1 CRIXNQKCFQ HLDDCCSXXC NXXNXCV 

(HITS-AT: 1-17)

NTE

type	loca	tion	description	
uncommon	Hyp-4		_	
uncommon	Aaa-18	_	-	
uncommon	Aaa-19	_	-	
uncommon	Aaa-22	_	<del>-</del> .	
uncommon	Aaa-23	_	_	
uncommon	Aaa-25	_	-	

ANSWER 2 OF 12 REGISTRY COPYRIGHT 2003 ACS

331640-80-3 REGISTRY - CA answer #3

L-Alanine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-Lasparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-Lhistidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L- $\verb|cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl$ phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFNKCA 

```
CHITS AT: 1-17 )
```

NTE

type ----- location ----- description

bridge Cys-1 - Cys-16 disulfide bridge
bridge Cys-8 - Cys-20 disulfide bridge
bridge Cys-15 - Cys-26 disulfide bridge
uncommon Hyp-4 - -

L2 ANSWER 3 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-76-7 J REGISTRY CA reference #3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-phenylalanyl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-alanyl-L-lysyl-L-cysteinyl-, cyclic (1.fwdarw.16),(8.fwdarw.20),(15.fwdarw.26)-tris(disulfide) (9CI) (CA INDEX NAME)

SQL 27

## SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFAKCV

\_\_\_\_\_

HITS AT: 1-17)

NTE

type	lo	cation	description
bridge bridge bridge uncommon	Cys-1 Cys-8 Cys-15 Hyp-4	- Cys-16 - Cys-20 - Cys-26	disulfide bridge disulfide bridge disulfide bridge -

L2 ANSWER 4 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-75-6 REGISTRY CA reference # 3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-alpha.-aspartyl-L-alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-arginyl-L-phenylalanyl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA INDEX NAME)

SQL 27

SEQ 1 CRIXNQKCFQ HLDDCCARKC NRFNKCV

\_\_\_\_\_\_\_\_\_\_

HITS AT: 1-17 >

NTE

type	lo	cation	description	
bridge bridge bridge uncommon	Cys-1 Cys-8 Cys-15 Hyp-4	- Cys-16 - Cys-20 - Cys-26	disulfide bridge disulfide bridge disulfide bridge	

L2 ANSWER 5 OF 12 REGISTRY COPYRIGHT 2003 ACS

RN 331640-74-52 REGISTRY CA reference #3

CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-

```
{\tt asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-Cysteinyl-L-cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteinyl-Cysteiny
                  histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
                   cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-alanyl-L-arginyl-L-
                  phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
                    (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI)
                   INDEX NAME)
    SOL
                  27
    SEO
                              1 CRIXNQKCFQ HLDDCCSRKC ARFNKCV
                                    HITS AT: 1-17 3
    ----- location ----- description
     bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -
                 ANSWER 6 OF 12 REGISTRY COPYRIGHT 2003 ACS
   L2
   RN
                331640-69-80 REGISTRY CA reference #3
   CN
                 L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-
                  asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-tyrosyl-L-glutaminyl-L-
                  histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
                  cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-
                  phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
                  (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI)
                  INDEX NAME)
   SQL
               27
  SEO
                              1 CRIXNQKCYQ HLDDCCSRKC NRFNKCV
  HITS AT:
                             1-177
  NTE
     type ----- location ----- description
    bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -
          ANSWER 7 OF 12 REGISTRY COPYRIGHT 2003 ACS 331640-66-5 REGISTRY CA reference #3
[RN]
                L-Valine, L-cysteinyl-L-lysyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-
  CN
                 {\tt asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-phenylalanyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminyl-L-glutaminy
                 histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
                 cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-
                 phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
                 (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA
                 INDEX NAME)
  SOL
               27
  SEO
                             1 CKIXNQKCFQ HLDDCCSRKC NRFNKCV
                                  HITS AT: 1-17 >
```

----- location ----- description

• . . . . .

```
bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -
   ANSWER 8 OF 12 REGISTRY COPYRIGHT 2003 ACS
L2
RN 331640=65=4 REGISTRY CA reference # 3
    L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-
    asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-
    histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
     cysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-
    phenylalanyl-L-asparaginyl-L-alanyl-L-cysteinyl-, cyclic (1.fwdarw.16),(8.fwdarw.20),(15.fwdarw.26)-tris(disulfide) (9CI) (CA
     INDEX NAME)
SOL
    27
        1 CRIXNOKCFQ HLDDCCSRKC NRFNACV
SEQ
          HITS_AT: 1-17 2
NTE
----- location ----- description
bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -
_____
   ANSWER 9 OF 12 REGISTRY COPYRIGHT 2003 ACS 331640-62-1 2 REGISTRY CA reference #3
T.2
RN
     L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-
     asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-
     histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-L-
     cysteinyl-L-seryl-L-arginyl-L-alanyl-L-cysteinyl-L-asparaginyl-L-arginyl-L-
     phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic
     (1.fwdarw.16),(8.fwdarw.20),(15.fwdarw.26)-tris(disulfide)(9CI)(CA
     INDEX NAME)
SQL 27
         1 CRIXNQKCFQ HLDDCCSRAC NRFNKCV
SEQ
          ______
HITS AT: - 1-17 3
NTE
______
        ----- location ----- description
 bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -
 L2 ANSWER 10 OF 12 REGISTRY COPYRIGHT 2003 ACS
RN 331640-60-95 REGISTRY CA reference #3
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CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-histidyl-L-leucyl-L-alpha.-aspartyl-L-alpha.-aspartyl-L-cysteinyl-L-cysteinyl-L-cysteinyl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-alanyl-L-phenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA INDEX NAME)

Kam 09/666837

Page 5

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SQL 27
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SEQ 1 CRIXNQKCFQ HLDDCCSRKC NAFNKCV --------HITS AT: 1-17 3 ----- location ----- description . bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -ANSWER 11 OF 12 REGISTRY COPYRIGHT 2003 ACS 331640=59=6 REGISTRY CA reference # 3 RN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L-CN asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-Lhistidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-Lcysteinyl-L-seryl-L-alanyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-Lphenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26)-tris(disulfide) (9CI) (CA INDEX NAME) 27 SQL 1 CRIXNQKCFQ HLDDCCSAKC NRFNKCV SEO HITS AT: 1-17 type ----- location ----- description -bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -ANSWER 12 OF 12 REGISTRY COPYRIGHT 2003 ACS RN 196605-79-5) REGISTRY CA references 1-11 CN .kappa.-Conotoxin P VIIA (9CI) (CA INDEX NAME) OTHER NAMES: CN L-Valine, L-cysteinyl-L-arginyl-L-isoleucyl-(4R)-4-hydroxy-L-prolyl-L- ${\tt asparaginyl-L-glutaminyl-L-lysyl-L-cysteinyl-L-phenylalanyl-L-glutaminyl-L-glutaminy$ histidyl-L-leucyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-cysteinyl-Lcysteinyl-L-seryl-L-arginyl-L-lysyl-L-cysteinyl-L-asparaginyl-L-arginyl-Lphenylalanyl-L-asparaginyl-L-lysyl-L-cysteinyl-, cyclic (1.fwdarw.16), (8.fwdarw.20), (15.fwdarw.26) -tris(disulfide) SQL SEQ 1 CRIXNQKCFQ HLDDCCSRKC NRFNKCV HITS AT: 1-17 7 ----- location ----- description bridge Cys-1 - Cys-16 disulfide bridge bridge Cys-8 - Cys-20 disulfide bridge bridge Cys-15 - Cys-26 disulfide bridge uncommon Hyp-4 -

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This file contains CAS Registry Numbers for easy and accurate substance identification.

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ANSWER 1 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:

2002:420792 CAPLUS

DOCUMENT NUMBER:

137:136264

TITLE:

Inhibition of single Shaker K channels by

.kappa.-conotoxin-PVIIA

AUTHOR(S):

Naranjo, David

CORPORATE SOURCE:

Instituto de Fisiologia Celular, Universidad Nacional Autonoma de Mexico, Circuito Exterior, Mexico, 04510,

SOURCE:

Biophysical Journal (2002), 82(6), 3003-3011

CODEN: BIOJAU; ISSN: 0006-3495

PUBLISHER:

Biophysical Society

DOCUMENT TYPE: Journal LANGUAGE: English

.kappa.-Conotoxin-PVIIA (.kappa.-PVIIA) is a 27-residue basic (+4) peptide from the venom of the predator snail Conus purpurascens. A single .kappa.-PVIIA mol. interrupts ion conduction by binding to the external mouth of Shaker K channels. The blockade of Shaker by .kappa.-PVIIA was studied at the single channel level in membrane patches from Xenopus oocytes. The amplitudes of blocked and closed events were undistinguishable, suggesting that the toxin interrupts ion conduction completely. Between -20 and 40 mV .kappa.-PVIIA increased the latency to the first opening by one order of magnitude in a concn.-independent fashion. Because .kappa.-PVIIA has higher affinity for the closed channels at high enough concn. to block >90% of the resting channels, the dissocn. rate could be estd. from the anal. of the first latency. At 0 mV, the dissocn. rate was 20 s-1 and had an effective valence of 0.64. The apparent closing rate increased linearly with [.kappa.-PVIIA] indicating an assocn. rate of 56 .mu.M-1 s-1. The toxin did not modify the fraction of null traces. This result suggests that the structural rearrangements in the external mouth contributing to the slow inactivation preserve the main geometrical features of the toxin-receptor interaction.

Kam 09/666837 Use Registry # to match citation to sequence in Registry record

196605-79-5, .kappa.-Conotoxin-PVIIA

RL: BSU (Biological study, unclassified); BIOL (Biological study) (inhibition of single Shaker K channels by .kappa.-conotoxin-PVIIA)

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 2 OF 11 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2001:872474 CAPLUS

DOCUMENT NUMBER:

136:258891

TITLE:

Molecular simulation of the interaction of

.kappa.-conotoxin-PVIIA with the Shaker potassium

channel pore

AUTHOR(S):

Moran, Oscar

CORPORATE SOURCE:

CNR, Istituto di Cibernetica e Biofisica, Genoa,

16149, Italy

SOURCE:

European Biophysics Journal (2001), 30(7), 528-536

CODEN: EBJOE8; ISSN: 0175-7571

PUBLISHER:

Springer-Verlag

DOCUMENT TYPE:

Journal

LANGUAGE:

English Mol. simulation techniques were applied to predict the interaction of the voltage-dependent Shaker potassium channel with the channel-blocking toxin .kappa.-conotoxin-PVIIA (PVIIA). A structural three-dimensional model of the extracellular vestibule of the potassium channel was constructed based on structural homologies with the bacterial potassium channel Kcsa, whose structure has been solved by x-ray crystallog. The docking of the PVIIA mol. was obtained by a geometric recognition algorithm, yielding 100 possible conformations. A series of residue-residue distance restraints, predicted from mutation-cycle expts., were used to select a small set of a plausible channel-toxin complex models among the resulting possible conformations. The four final conformations, with similar characteristics, can explain most of the single-point mutation expts. done with this system. The models of the Shaker-PVIIA interaction predict two clusters of amino acids, crit. for the binding of the toxin to the channel. The first cluster is the amino acids R2, I3, Q6 and K7 that form the plug of the toxin that interacts with the entrance to the selectivity filter of the channel. The second cluster of residues, R22, F23, N24 and K25, interacts with a channel region near to the external entrance of the pore vestibule. The consistency of the obtained models and the exptl. data indicate that the Shaker-PVIIA complex model is reasonable and can be used in further biol. studies such as the rational design of blocking agents of potassium channels and the mutagenesis of both toxins and potassium channels.

196605-79-5, .kappa.-Conotoxin-PVIIA

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(complexes with potassium channel; mol. simulation of the interaction of .kappa.-conotoxin-PVIIA with the Shaker potassium channel pore) REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 3 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:

2001:228916 CAPLUS

DOCUMENT NUMBER:

134:275775

TITLE:

.kappa.-Conotoxin PVIIA and analogs and derivatives for activating ATP-sensitive potassium channels, and

therapeutic use

INVENTOR(S):

Cornell-Bell, Ann H.; Pemberton, Karen E.; Temple, Davis L., Jr.; Layer, Richard T.; McCabe, R. Tyler;

Jones, Robert R.

PATENT ASSIGNEE(S): SOURCE:

Cognetix, Inc., USA PCT Int. Appl., 46 pp.

CODEN: PIXXD2

DOCUMENT TYPE: LANGUAGE: Patent English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

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APPLICATION NO. DATE
     PATENT NO.
                      KIND DATE
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                              20010329
                                             WO 2000-US25827 20000921
     WO 2001021648
                       A1
         W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
              SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,
              ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
              DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
              CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
                                             EP 2000-965219
                       A1 20020703
                                                                20000921
     EP 1218407
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, SI, LT, LV, FI, RO, MK, CY, AL
                                           US 1999-155135P P 19990922
PRIORITY APPLN. INFO.:
                                           US 2000-219438P P 20000720
                                            WO 2000-US25827 W 20000921
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OTHER SOURCE(S): MARPAT 134:275775

The invention relates to uses of .kappa.-conotoxin PVIIA, analogs and derivs. for activating ATP-sensitive potassium channels. The activation of ATP-sensitive potassium channels is useful for opening KATP channels which can be used to treat a wide range of disease and injury states, including cerebral and cardiac ischemia and asthma.

331640-59-6 331640-59-6D, derivs. 331640-60-99 331640-60-9D, derivs. 331640-62-1 331640-62-1D) , derivs. 331640-65-4 331640-65-4D, derivs. 331640-66-5 331640-66-5D, derivs. 331640-69-89 331640-69-8D, derivs. 331640-74-5 331640-74-5D) , derivs. 331640-75-6 331640-75-6D, derivs. 331640-76-7 331640-76-7D, derivs. 331640-80-39 331640-80-3D, derivs. 332843-22-89

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(.kappa.-conotoxin PVIIA and analogs and derivs. for activating ATP-sensitive potassium channels, and therapeutic use)

IT 196605-79-5,) .kappa.-CONOTOXIN P VIIA 196605-79-5D,)

.kappa.-CONOTOXIN P VIIA, analogs and derivs.

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(.kappa.-conotoxin PVIIA and analogs and derivs. for activating ATP-sensitive potassium channels, and therapeutic use)

ATP-sensitive potassium channels, and therapeutic use)
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AV

THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:579029 CAPLUS

DOCUMENT NUMBER: 133:292139

TITLE: Single amino acid substitutions in .kappa.-Conotoxin PVIIA disrupt interaction with the Shaker K+ channel

AUTHOR(S): Jacobsen, Richard B.; Koch, E. Dietlind;

Lange-Malecki, Bettina; Stocker, Martin; Verhey, Janko; Van Wagoner, Ryan M.; Vyazovkina, Alexandra;

Olivera, Baldomero M.; Terlau, Heinrich

CORPORATE SOURCE: Departments of Biology and Medicinal Chemistry, University of Utah, Salt Lake City, UT, 84112, USA

Kam 09/666837 Page 9

SOURCE:

Journal of Biological Chemistry (2000), 275(32),

24639-24644

CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER:

American Society for Biochemistry and Molecular

Biology

DOCUMENT TYPE: LANGUAGE:

Journal English

AB .kappa.-Conotoxin PVIIA (.kappa.-PVIIA), a 27-amino acid peptide with three disulfide crosslinks, isolated from the venom of Conus purpurascens, is the first conopeptide shown to inhibit the Shaker K+ channel. Recently, two groups independently detd. the soln. structure for .kappa.-PVIIA using NMR; although the structures reported were similar, two mutually exclusive models for the interaction of the peptide with the Shaker channel were proposed. The authors carried out a structure/function anal. of .kappa.-PVIIA, with alanine substitutions for all amino acids postulated to be key residues by both groups. The authors' data are consistent with the crit. dyad model developed by Menez and co-workers for polypeptide antagonists of K+ channels. In the case of

.kappa.-PVIIA, Lys7 and Phe9 are essential for activity as predicted by Savarin et al. these workers also correctly predicted an important role for Lys25. Thus, although .kappa.-conotoxin PVIIA has no obvious sequence homol. to polypeptide toxins from other venomous animals that interact with voltage-gated K+ channels, there may be convergent functional features in diverse K+ channel polypeptide antagonists.

IT 196605-79-5) .kappa.-Conotoxin P VIIA

RL: ADV (Adverse effect, including toxicity); PRP (Properties); BIOL (Biological study)

(single amino acid substitutions in .kappa.-Conotoxin PVIIA disrupt interaction with the Shaker K+ channel)

REFERENCE COUNT:

28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 5 OF 11 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2000:191100 CAPLUS

DOCUMENT NUMBER:

132:237373

TITLE: Preparation of cyclized conotoxin peptides INVENTOR(S): Craik, David James; Daly, Norelle Lee; Nielsen,

Katherine Justine

PATENT ASSIGNEE(S): University of Queensland, Australia

SOURCE: PCT Int. Appl., 43 pp.

CODEN: PIXXD2

DOCUMENT TYPE: LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PA	rent	NO.		KI	ND	DATE			А	PPLI	CATI	ON N	٥.	DATE			
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		SL,	ТJ,	TM,	TR,	TT,	TZ,	UA,	UG,	US,	UZ,	VN,	YU,	ZA,	ZW,	AM,	AZ,
		BY,	KG,	KZ,	MD,	RU,	ТJ,	TM								-	·
	RW:													BE,			
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														NL,		MC,	PT,
						FI,						•	•	•	•	•	•

PRIORITY APPLN. INFO.:

AU 1998-5895 A 19980914 W 19990914 WO 1999-AU769

Cyclized conotoxin peptides were prepd. for the therapeutic treatment of mammals. Thus, cyclo[CKGKGAKCSRLMYDCCTGSCRSGKCTRNGLPG], a cyclic analog of MVIIA having the linking moiety TRNGLPG, was prepd. by the solid-phase method.

ΙT 196605-79-5DP, j.kappa.-Conotoxin P VIIA, cyclic analogs RL: SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(prepn. of cyclized conotoxin peptides)

REFERENCE COUNT: THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 6 OF 11 CAPLUS COPYRIGHT 2003 ACS

1999:477426 CAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 131:253554

A marine snail neurotoxin shares with scorpion toxins TITLE:

a convergent mechanism of blockade on the pore of

voltage-gated K channels

Garcia, Esperanza; Scanlon, Martin; Naranjo, David AUTHOR(S): CORPORATE SOURCE:

Centro de Investigaciones Biomedicas, Universidad de

Colima, Colima, 28045, Mex.

Journal of General Physiology (1999), 114(1), 141-157 SOURCE:

CODEN: JGPLAD; ISSN: 0022-1295

Rockefeller University Press PUBLISHER:

DOCUMENT TYPE: Journal LANGUAGE: English

.kappa.-Conotoxin-PVIIA (.kappa.-PVIIA) belongs to a family of peptides ΑB derived from a hunting marine snail that targets to a wide variety of ion channels and receptors. .kappa.-PVIIA is a small, structurally constrained, 27-residue peptide that inhibits voltage-gated K channels. Three disulfide bonds shape a characteristic four-loop folding. The spatial localization of pos. charged residues in .kappa.-PVIIA exhibits strong structural mimicry to that of charybdotoxin, a scorpion toxin that occludes the pore of K channels. The authors studied the mechanism by which this peptide inhibits Shaker K channels expressed in Xenopus oocytes with the N-type inactivation removed. Chronically applied to whole oocytes or outside-out patches, .kappa.-PVIIA inhibition appears as a voltage-dependent relaxation in response to the depolarizing pulse used to activate the channels. At any applied voltage, the relaxation rate depended linearly on the toxin concn., indicating a bimol. stoichiometry. Time consts. and voltage dependence of the current relaxation produced by chronic applications agreed with that of rapid applications to open channels. Effective valence of the voltage dependence, z.delta., is .apprx.0.55 and resides primarily in the rate of dissocn. from the channel, while the assocn. rate is voltage independent with a magnitude of 107-108 M-1s-1, consistent with diffusion-limited binding. Compatible with a purely competitive interaction for a site in the external vestibule, tetraethylammonium, a well-known K-pore blocker, reduced .kappa.-PVIIA's assocn. rate only. Removal of internal K+ reduced, but did not eliminate, the effective valence of the toxin dissocn. rate to a value <0.3. This trans-pore effect suggests that: (a) as in the .alpha.-KTx, a pos. charged side chain, possibly a Lys, interacts electrostatically with ions residing inside the Shaker pore, and (b) a part of the toxin occupies an externally accessible K+ binding site, decreasing the degree of pore occupancy by permeant ions. The authors conclude that, although evolutionarily distant to scorpion toxins, .kappa.-PVIIA shares with them a remarkably similar mechanism of inhibition of K channels.

ΙT 196605-79-5, ). kappa. -Conotoxin-PVIIA

> RL: ADV (Adverse effect, including toxicity); BIOL (Biological study) (neurotoxin of marine snail shares with scorpion toxins a convergent mechanism of blockade on the pore of voltage-gated K (potassium)

Kam 09/666837 Page 11

channels)

61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 7 OF 11 CAPLUS COPYRIGHT 2003 ACS 1999:477425 CAPLUS ACCESSION NUMBER:

131:253553 DOCUMENT NUMBER:

TITLE: The block of Shaker K+ channels by .kappa.-conotoxin

PVIIA is state dependent

AUTHOR(S): Terlau, Heinrich; Boccaccio, Anna; Olivera, Baldomero

M.; Conti, Franco

Max-Planck-Institut fur Experimentelle Medizin, CORPORATE SOURCE:

Gottingen, 37075, Germany

Journal of General Physiology (1999), 114(1), 125-140 SOURCE:

CODEN: JGPLAD; ISSN: 0022-1295 Rockefeller University Press

PUBLISHER: DOCUMENT TYPE: Journal

English LANGUAGE:

.kappa.-Conotoxin PVIIA is the first conotoxin known to interact with voltage-gated potassium channels by inhibiting Shaker-mediated currents. The authors studied the mechanism of inhibition and concluded that PVIIA blocks the ion pore with a 1:1 stoichiometry and that binding to open or closed channels is very different. Open-channel properties are revealed by relaxations of partial block during step depolarizations, whereas double-pulse protocols characterize the slower reequilibration of closed-channel binding. In 2.5 mM-[K+]o, the IC50 rises from a tonic value of .apprx.50 to .apprx.200 nM during openings at 0 mV, and it increases e-fold for about every 40-mV increase in voltage. The change involves mainly the voltage dependence and a 20-fold increase at 0 mV of the rate of PVIIA dissocn., but also a fivefold increase of the assocn. rate. PVIIA binding to Shaker .DELTA.6-46 channels lacking N-type inactivation or to wild phenotypes appears similar, but inactivation partially protects the latter from open-channel unblock. Raising [K+]o to 115 mM has little effect on open-channel binding, but increases almost 10-fold the tonic IC50 of PVIIA due to a decrease by the same factor of the toxin rate of assocn. to closed channels. In analogy with charybdotoxin block, the authors attribute the acceleration of PVIIA dissocn. from open channels to the voltage-dependent occupancy by K+ ions of a site at the outer end of the conducting pore. The authors also argue that the occupancy of this site by external cations antagonizes on binding to closed channels, whereas the apparent competition disappears in open channels if the competing cation can move along the pore. It is concluded that PVIIA can also be a valuable tool for probing the state of ion permeation inside the pore.

IT \196605=79-5\, .kappa.-Conotoxin PVIIA

RL: ADV (Adverse effect, including toxicity); BIOL (Biological study) (shaker K+ (potassium) channels block by .kappa.-conotoxin PVIIA is state dependent)

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 8 OF 11 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 1998:276339 CAPLUS

DOCUMENT NUMBER: 129:37385

TITLE: Three-dimensional structure of .kappa.-conotoxin

PVIIA, a novel potassium channel-blocking toxin from

cone snails

AUTHOR(S): Savarin, Philippe; Guenneugues, Marc; Gilquin,

Bernard; Lamthanh, Hung; Gasparini, Sylvanie;

Zinn-Justin, Sophie; Menez, Andre

CORPORATE SOURCE: CE Saclay, Dep. Ing. Et. Proteines, CEA,

Gif-sur-Yvette, 91191, Fr.

SOURCE: Biochemistry (1998), 37(16), 5407-5416 Kam 09/666837 Page 12

CODEN: BICHAW; ISSN: 0006-2960 American Chemical Society

DOCUMENT TYPE: Journal LANGUAGE: English

PUBLISHER:

AUTHOR(S):

AB .kappa.-Conotoxin PVIIA from the venom of Conus purpurascens is the first cone snail toxin that was described to block potassium channels. We synthesized chem. this toxin and showed that its disulfide bridge pattern is similar to those of .omega.- and .delta.-conotoxins. .kappa.-Conotoxin competes with radioactive .alpha.-dendrotoxin for binding to rat brain synaptosomes, confirming its capacity to bind to potassium channels; however, it behaves as a weak competitor. The three-dimensional structure of .kappa.-conotoxin PVIIA, as elucidated by NMR spectroscopy and mol. modeling, comprises two large parallel loops stabilized by a triple-stranded antiparallel .beta.-sheet and three disulfide bridges. The overall fold of .kappa.-conotoxin is similar to that of calcium channel-blocking .omega.-conotoxins but differs from those of potassium channel-blocking toxins from sea anemones, scorpions, and snakes. Local topogs. of .kappa.-conotoxin PVIIA that might account for its capacity to recognize Kv1-type potassium channels are discussed.

IT 196605=79-5P,2 .kappa.-Conotoxin PVIIA

RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation) (three-dimensional structure of .kappa.-conotoxin PVIIA, novel potassium channel-blocking toxin from cone snails)

L3 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:60152 CAPLUS

DOCUMENT NUMBER: 128:137369

TITLE: Solution structure and proposed binding mechanism of a

novel potassium channel toxin .kappa.-conotoxin PVIIA Scanlonl, Martin J.; Naranjo, David; Thomas, Linda; Alewood, Paul F.; Lewis, Richard J.; Craik, David J.

CORPORATE SOURCE: Centre for Drug Design, University of Queensland, St.

Lucia, 4072, Australia

SOURCE: Structure (London) (1997), 5(12), 1585-1597

CODEN: STRUE6; ISSN: 0969-2126

PUBLISHER: Current Biology Ltd.

DOCUMENT TYPE: Journal LANGUAGE: English

AB The three-dimensional structure of PVIIA resembles the triple- stranded .beta. sheet/cystine-knot motif formed by a no. of toxic and inhibitory peptides. Subtle structural differences, predominantly in loops 2 and 4, are obsd. between PVIIA and other conotoxins with similar structural frameworks, however. Electrophysiol. binding data suggest that PVIIA blocks channel currents by binding in a voltage-sensitive manner to the external vestibule and occluding the pore. Comparison of the electrostatic surface of PVIIA with that of the well-characterized potassium channel blocker charybdotoxin suggests a likely binding orientation for PVIIA. Although the structure of PVIIA is considerably different to that of the .alpha.K scorpion toxins, it has a similar mechanism of channel blockade. On the basis of a comparison of the structures of PVIIA and charybdotoxin, we suggest that Lys19 of PVIIA is the residue which is responsible for phys. occluding the pore of the potassium channel.

IT 196605-79-50 .kappa.-Conotoxin PVIIA

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (soln. structure and potassium channel blocking activity of .kappa.-conotoxin PVIIA)

L3 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1998:39008 CAPLUS

DOCUMENT NUMBER: 128:111749

TITLE: .kappa.-Conotoxin PVIIA is a peptide inhibiting the

09/666837 Kam

Page 13

Shaker K+ channel

AUTHOR(S): Shon, Ki-Joon; Stocker, Martin; Terlau, Heinrich;

Stuhmer, Walter; Jacobsen, Richard; Walker, Craig; Grilley, Michelle; Watkins, Maren; Hillyard, David R.;

Gray, William R.; Olivera, Baldomero M.

Department of Physiology and Biophysics, Case Western CORPORATE SOURCE:

Reserve University, Cleveland, OH, 44106, USA

Journal of Biological Chemistry (1998), 273(1), 33-38 CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular

Biology

DOCUMENT TYPE: Journal LANGUAGE: English

SOURCE:

AΒ .kappa.-Conotoxin PVIIA (.kappa.-PVIIA), a 27-amino acid toxin from Conus purpurascens venom that inhibits the Shaker potassium channel, was chem. synthesized in a biol. active form. The disulfide connectivity of the peptide was detd. This is the first Conus peptide known to target K+ channels. Although the Shaker K+ channel is sensitive to .kappa.-PVIIA, the rat brain Kv1.1 subtype is resistant. Chimeras between Shaker and the Kv1.1 K+ channels were constructed and expressed in Xenopus oocytes. Only channels contg. the putative pore-forming region between the fifth and sixth transmembrane domains of Shaker retained toxin sensitivity, indicating that the toxin target site is in this region of the channel. Evidence is presented that .kappa.-PVIIA interacts with the external tetraethyl-ammonium binding site on the Shaker channel. Although both .kappa.-PVIIA and charybdotoxin inhibit the Shaker channel, they must interact differently. The F425G Shaker mutation increases charybdotoxin affinity by 3 orders of magnitude but abolishes .kappa.-PVIIA sensitivity. The precursor sequence of .kappa.-PVIIA was deduced from a cDNA clone, revealing a prepropeptide comprising 72 amino acids. The N-terminal region of the .kappa.-PVIIA prepropeptide exhibits striking homol. to the .omega.-, .mu.O-, and .delta.-conotoxins. Thus, at least four pharmacol. distinct superfamilies of Conus peptides belong to the same "O" superfamily, with the .omega. - and .kappa. - conotoxins forming one branch, and the .delta. - and .mu.O-conotoxins forming a second major branch. IT

196605-79-5P .kappa.-Conotoxin PVIIA RL: PRP (Properties); PUR (Purification or recovery); PREP (Preparation) (.kappa.-Conotoxin PVIIA inhibition of Shaker K+ channel)

ANSWER 11 OF 11 CAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 1997:640695 CAPLUS

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TITLE: Conotoxin peptide PVIIa

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CA 2248710	AA 19970925	CA 1997-2248710	19970314
AU 9720690	A1 19971010	AU 1997-20690	19970314
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An ew peptide, .kappa.-conotoxin PVIIA, is disclosed. This peptide is found naturally in the cone snail Conus purpurascens and has the amino acid sequence Cys-Arg-Ile-Xaa-Asn-Gln-Lys-Cys-Phe-Gln-His-Leu-Asp-Asp-Cys-Cys-Ser-Arg-Lys-Cys-Asn-Arg-Phe-Asn-Lys-Cys-Val where Xaa represents 4-trans-hydroxyproline, hydroxyproline or proline. This peptide together with a previously disclosed peptide, .delta.-conotoxin PVIA, act synergistically to rapidly immobilize fish which are injected with the two peptides. Injection of .kappa.-conotoxin PVIIA alone results in different symptoms with an injected fish becoming hyperactive and then contracting and suddenly extending all major fins. This fin-popping occurs repeatedly resulting in a series of jerky movements, but injection of only .kappa.-conotoxin PVIIA does not immobilize or kill the fish.

IT (196605-79-5P,).kappa.-Conotoxin P VIIA
RL: ADV (Adverse effect, including toxicity); PRP (Properties); PUR
(Purification or recovery); BIOL (Biological study); PREP (Preparation)
(conotoxin peptide PVIIa)

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